

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:33 ; Search time 3691.27 Seconds
(without alignments)
8940.469 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867
Sequence: 1 agcaccacgagagcgtgaga.....ccctactcagaagaagcgcta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:

1: gb_eat1:*
2: gb_eat2:*
3: gb_hcc:*
4: gb_eat3:*
5: gb_eat4:*
6: gb_eat5:*
7: gb_eat6:*
8: gb_gaet1:*
9: gb_gaet2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110.8	12.8	466	8	AQ229478 HS_2021.A
2	109.2	12.6	680	9	AG186502 Pan trolg1
3	107.6	12.4	418	8	AQ390169 CITR1-El-
4	107.2	12.4	469	4	BM509394 1h17f10.Y
5	107.2	12.4	516	4	BI468297 1d87b01.Y
6	107.2	12.4	529	5	BQ270800 1k05b06.Y
7	107.2	12.4	556	5	BQ267333 1k02c03.Y
8	107.2	12.4	578	7	CR825308 1k02c03.Y
9	107.2	12.4	584	5	BU071662 1m32a11.Y
10	107.2	12.4	584	5	BU782096 1m99h05.Y
11	107.2	12.4	589	5	BQ270346 1k09g10.Y
12	107.2	12.4	589	5	BU783590 1m06g04.Y
13	106.8	12.3	564	5	BX507946 DKP2p686L
14	106.4	12.3	635	8	AQ428429 CITR1-El-
15	106.4	12.2	679	6	CA428584 UI-H-FEL-
16	106.4	12.2	774	8	AQ751486 HS_5576.B
17	104.8	12.1	671	8	AQ418931 RPCI-11-1
18	104.6	12.1	465	5	AQ527107 CITR1-El-
19	104.6	12.1	815	5	BQ429052 AGENCOURT
20	104.4	12.0	303	4	BM672404 UI-E-CO-
21	104.4	12.0	473	5	BZ599186 WHACR10TF
22	104.4	12.0	595	8	BX099082 BX099082
23	104.4	12.0	712	9	AG139751 Pan trolg1
24	104.4	12.0	805	8	BZ604439 WHAAJ34TR

25	104	12.0	516	7	CN276447	CN276447 170006001
26	103.8	12.0	451	7	N66929	N66929 za47h09.a1
27	103.6	11.9	550	6	CB163810	CB163810 K-EST0224
28	103	11.9	837	4	BI820230	BI820230 603037070
29	103	11.9	1074	5	BQ429712	BQ429712 AGENCOURT
30	102.8	11.9	318	4	BI492686	BI492686 df27g08.w
31	102.8	11.9	340	2	AM021747	AM021747 df27g08.Y
32	102.8	11.9	608	7	CN411496	CN411496 170005332
33	102.8	11.9	684	9	AG109444	AG109444 Pan trolg1
34	102.2	11.8	1614	3	CR603212	CR603212 full-1eng
35	102	11.8	364	8	AQ333390	AQ333390 HS_5010.A
36	102	11.8	499	6	CD694607	CD694607 EST11130
37	101.6	11.7	256	1	AA084337	AA084337 zn04B05..B
38	101.2	11.7	382	1	AV764523	AV764523 AV764523
39	101.2	11.7	474	1	AI866580	AI866580 t251c10.X
40	101.2	11.7	514	8	B37536	B37536 HS-104-A1-
41	101.2	11.7	735	1	AU120382	AU120382 AU120382
42	101.2	11.7	773	4	BG221771	BG221771 RST41586
43	101.2	11.7	815	2	BF382750	BF382750 601816513
44	101.2	11.7	859	8	AO750588	AO750588 HS_5573.B
45	101.2	11.7	867	5	BUB53592	BUB53592 AGENCOURT

ALIGNMENTS

RESULT 1
AQ229478/c
LOCUS
DEFINITION
HS_2021.A2 A08 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2021 Col-16 Row-A, genomic survey
sequence.

ACCESSION
AQ229478
VERSION
AQ229478.1 GI:3654707
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Mahalir, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kellner, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE
99380589
PUBMED
10449764
COMMENT
Contact: Mahalir GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2021 row: A column: 16
Class: BAC ends
High quality sequence stop: 466.
Location/Qualifiers

FEATURES
source
1..466
location/Qualifiers

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2021 Col=16 Row=A"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11, BAC clones in E-Coli DH10B"

ORIGIN
Query Match 12.8%; Score 110.8; DB 8; Length 466;
Best Local Similarity 90.8%; Pred. No. 5.6e-17;

Matches 118; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTTGAGACAGAGATGCTTGAACCCGGAGGAGGTTGCAGTG 60
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 Db 399 AGCTACTCAGAGGCTTGAGAGAGATGCTTGAACCCGGAGGAGGTTGCAGTG 340
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QY 61 AGCCGAGATCAGCCGCTAGATCTCATCCAGCCGCGGAAAGAGCAAGACTCCGCTCA 120
 |||||
 Db 339 AGCCGAGATCAGCCGCTAGATCTCATCCAGCATGGAGACAGCAAGACTCCGCTCA 280
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QY 121 AAAAAAAAAA 130
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 Db 279 AAAAAAAAAA 270
 |||||

RESULT 2
 LOCUS AG186502 680 bp DNA linear GSS 09-JAN-2002
 DEFINITION Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
 sequence.
 ACCESSION AG186502
 VERSION AG186502.1 GI:16716182
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Tokoki, Y., Watanabe, H., and Sakaki, Y.
 BAC end sequences of library RP43-43
 Unpublished
 2 (bases 1 to 680)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Tokoki, Y., Watanabe, H., and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RP43-43 This BAC
 end was generated during the RAD process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..680
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-060015.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_1ib="RP43-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 12.6%; Score 109.2; DB 9; Length 680;
 Best Local Similarity 87.0%; Pred. No. 1.4e-16;
 Matches 120; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 121 AAAAAAAAAATCATTACA 138
 |||||
 Db 359 AAAAAAAAAAGAAAAA 376
 |||||

RESULT 3
 LOCUS AQ390169 418 bp DNA linear GSS 06-MAR-1999
 DEFINITION CITR1-EI-2544A19.TF CITR1-EI Homo sapiens genomic clone 2544A19,
 genomic survey sequence.
 ACCESSION AQ390169
 VERSION AQ390169.1 GI:4361192
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Zhao, S., Adams, M.D., Niernan, W., Malek, J., Shizuya, H., Simon, M. and
 Venter, J.C.
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: CITR1-EI-2544A19.TF
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
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 1..418
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="2544A19"
 /sex="male"
 /cell_type="sperm"
 /clone_1ib="CITR1-EI"
 /note="Vector: pBelobAC11, Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"

ORIGIN
 Query Match 12.4%; Score 107.6; DB 8; Length 418;
 Best Local Similarity 86.2%; Pred. No. 3.6e-16;
 Matches 119; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 AGTACTCAGAGGCTTGAGACAGAGATGCTTGAACCCGGAGGAGGTTGCAGTG 60
 |||||
 Db 95 AGTACTCAGAGGCTTGAGAGAGATGCTTGAACCCGGAGGAGGTTGCAGTG 154
 |||||

QY 61 AGCCGAGATCAGCCGCTAGATCTCATCCAGCTGGCGGAAAGAGCAAGACTCCGCTCA 120
 |||||
 Db 155 AGCCGAGATCAGCCGCTAGATCTCATCCAGCTAGCAAGAGCAAGACTCCGCTCA 214
 |||||

QY 121 AAAAAAAAAATCATTACA 138
 |||||
 Db 215 AAAAAAAAAACAAAAA 232
 |||||

RESULT 4
 LOCUS BM509394 469 bp mRNA linear EST 15-FEB-2002
 DEFINITION h17f10.y1 Human insulinoma Homo sapiens cDNA 5' similar to
 SW:AL08_HUMAN P39195 ALU SUBFAMILY SX SEQUENCE CONTAMINATION
 WARNING ENTRY. [1], mRNA sequence.
 ACCESSION BM509394

VERSION BM509394.1 GI:18680537
 EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
 Lentsha, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Maria, M., Page, D., Wylie, T., Martin, J., Bliscain, A.,
 Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelashvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from GIBCO
 High quality sequence stop: 416.
 Location/Qualifiers
 1..469
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="Human insulinoma"
 /note="Torgan: pancreas; Vector: pBluescript SK-; Site_1:
 XhoI; Site_2: EcoRI; Constructed with lambda ZAPIT system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permut
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

ORIGIN
 Query Match 12.4%; Score 107.2; DB 4; Length 469;
 Best Local Similarity 81.6%; Pred. No. 4.5e-16;
 Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 1 AGCTACTGAGGAGGTGAGACACGAGATCGCTGACCCGGGAGAGAGGTGCAGG 60
DB 285 AGCCACTGGGAGGCTTTAAATGGGAGAAATCGCTTGAACCTGGAGGACAGAGGTGCAGG 344
QY 61 AGCCGAGATCAAGCAGCTAGACTCCATCCAGCTGGGCGAAAGAGCAAGACTCCGCTTCA 120
DB 345 AGCCGAGATCAAGCAGCTAGACTCCATCCAGCTGGGCGAAAGAGCAAGACTCCGCTTCA 404
QY 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152
DB 405 AAAAAAAAAAGTTAGAAAAATGCTGCTT 436
  
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RESULT 5
 BI468297
 LOCUS BI468297 516 bp mRNA linear EST 11-MAR-2002
 DEFINITION ik05b01.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5022649
 5', mRNA sequence.
 ACCESSION BI468297

VERSION BI468297.1 GI:15284406
 EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
 Lentsha, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Maria, M., Page, D., Wylie, T., Martin, J., Bliscain, A.,
 Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelashvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 High quality sequence stop: 457.
 Location/Qualifiers
 1..516
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:5022649"
 /tissue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="Human insulinoma"
 /note="Torgan: pancreas; Vector: pBluescript SK-; Site_1:
 XhoI; Site_2: EcoRI; Constructed with lambda ZAPIT system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permut
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

ORIGIN
 Query Match 12.4%; Score 107.2; DB 4; Length 516;
 Best Local Similarity 81.6%; Pred. No. 4.5e-16;
 Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 1 AGCTACTGAGGAGGTGAGACACGAGATCGCTGACCCGGGAGAGAGGTGCAGG 60
DB 285 AGCCACTGGGAGGCTTTAAATGGGAGAAATCGCTTGAACCTGGAGGACAGAGGTGCAGG 344
QY 61 AGCCGAGATCAAGCAGCTAGACTCCATCCAGCTGGGCGAAAGAGCAAGACTCCGCTTCA 120
DB 345 AGCCGAGATCAAGCAGCTAGACTCCATCCAGCTGGGCGAAAGAGCAAGACTCCGCTTCA 404
QY 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152
DB 405 AAAAAAAAAAGTTAGAAAAATGCTGCTT 436
  
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RESULT 6
 BQ270800
 LOCUS BQ270800 529 bp mRNA linear EST 15-JUL-2003
 DEFINITION ik05b06.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5779930
 5', mRNA sequence.
 ACCESSION BQ270800

VERSION BQ270800.1 GI:20495866
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 529)
 AUTHORS Melton, D., Brown, J., Keny, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bilestein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelshvili, R., Williams, T., Jackson, Y., and Bowers, Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Other_ESTRs: ik05b06.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. J. Ferrer In vivo mass-excised to pbluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 428.
 Location/Qualifiers
 1..529
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5779930"
 /issue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="Human Insulinoma"
 /note="Organ: pancreas; Vector: pbluescript SK-; Site: 1: XhoI; Site 2: EcoRI; Constructed with lambda ZAPIT system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pbluescript SK- by Dr. H. Inoue following the Washington University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
 ORIGIN
 Query Match 12.4%; Score 107.2; DB 5; Length 529;
 Best Local Similarity 81.6%; Pred. No. 4.6e-16;
 Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 Oy 1 AGCTACTCAGAGGCTTGAGACGACGAGAAATCGTTGAACCCGGAGCGAGAGTTGCATG 60
 Db 285 AGCCACTCGGAGGCTTAAATGAGAAATCGTTGAACCTGAGGCGAGAGTTGCATG 344
 Oy 61 AGCCGAGTCAAGCAGCTAGACTCATTCAGCTGGGGGAGAAAGACAAAGATCCGCTCA 120
 Db 345 AGCCGAGTCAAGCAGCTAGACTCATTCAGCTGGGGGAGAGAGAAAGATCCATCTCA 404
 Oy 121 AAAAAAAAAATCGTTACATTTATGTGATTT 152
 Db 405 AAAAAAAAAAGTTAGAAAAATGCTGCTT 436

5', mRNA sequence.
 ACCESSION BQ267333
 VERSION BQ267333.1 GI:20492398
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 556)
 AUTHORS Melton, D., Brown, J., Keny, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bilestein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelshvili, R., Williams, T., Jackson, Y., and Bowers, Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. J. Ferrer In vivo mass-excised to pbluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 428.
 Location/Qualifiers
 1..556
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5779589"
 /issue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="Human Insulinoma"
 /note="Organ: pancreas; Vector: pbluescript SK-; Site: 1: XhoI; Site 2: EcoRI; Constructed with lambda ZAPIT system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pbluescript SK- by Dr. H. Inoue following the Washington University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
 ORIGIN
 Query Match 12.4%; Score 107.2; DB 5; Length 556;
 Best Local Similarity 81.6%; Pred. No. 4.6e-16;
 Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 Oy 1 AGCTACTCAGAGGCTTGAGACGACGAGAAATCGTTGAACCCGGAGCGAGAGTTGCATG 60
 Db 285 AGCCACTCGGAGGCTTAAATGAGAAATCGTTGAACCTGAGGCGAGAGTTGCATG 344
 Oy 61 AGCCGAGTCAAGCAGCTAGACTCATTCAGCTGGGGGAGAAAGACAAAGATCCGCTCA 120
 Db 345 AGCCGAGTCAAGCAGCTAGACTCATTCAGCTGGGGGAGAGAGAAAGATCCATCTCA 404
 Oy 121 AAAAAAAAAATCGTTACATTTATGTGATTT 152
 Db 405 AAAAAAAAAAGTTAGAAAAATGCTGCTT 436

RESULT 7
 BQ267333 556 bp mRNA linear EST 15-JUL-2003
 LOCUS BQ267333
 DEFINITION ik02c03.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:5779589

RESULT 8
 CK825308 578 bp mRNA linear EST 11-MAR-2004
 LOCUS CK825308

DEFINITION IK02C03.y6 Human insulinoma Homo sapiens cDNA clone IMAGE:5779589
5', mRNA sequence.
ACCESSION CK825308
VERSION CK825308.1 GI:44842233
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 578)
AUTHORS Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bilestein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R., Williams, T., Jackson, Y. and Bowers, Y.
WashU-Harvard Pancreas EST Project
TITLE Unpublished (2000)
JOURNAL Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
COMMENT Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
This read is a 5' RESEQUENCE of a previously sequenced pancreas clone
This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40UP from Gibco.
FEATURES
source
1..578
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5779589"
/cissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site, 1: XhoI; Site 2: EcoRI; Constructed with lambda ZapII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN
Query Match 12.4%; Score 107.2; DB 7; Length 578;
Best Local Similarity 81.6%; Pred. No. 4.6e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 AGCTACTGAGAGGCTGAGACAGAGATCGTTGAACCCGGAGGAGAGGTTGCAATG 60
DB 285 AGCCACTGGGAGGCTTAAATGGAGAAATCGCTGAACCTGAGGAGGAGGTTGCAATG 344
QY 61 AGCCGAGATCAAGGCTGAGACAGAGATCGTTGAACCCGGAGGAGAGGTTGCAATG 120
DB 345 AGCCGAGATCAAGGCTGAGACAGAGATCGTTGAACCCGGAGGAGAGGTTGCAATG 404
QY 121 AAAAAAAAAATCGTTACATTTATGTTGATT 152
DB 405 AAAAAAAAAAGTTAGAAAAATGCTGCTT 436

RESULT 9
LOCUS BU071662 584 bp mRNA linear EST 27-AUG-2002
DEFINITION hm2a11.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6036764

ACCESSION BU071662
VERSION BU071662.1 GI:22512851
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 584)
AUTHORS Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Scaer, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bilestein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R., Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
TITLE Unpublished (2000)
JOURNAL Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
COMMENT Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 428.
FEATURES
source
1..584
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6036764"
/cissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site, 1: XhoI; Site 2: EcoRI; Constructed with lambda ZapII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN
Query Match 12.4%; Score 107.2; DB 5; Length 584;
Best Local Similarity 81.6%; Pred. No. 4.6e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 AGCTACTGAGAGGCTGAGACAGAGATCGTTGAACCCGGAGGAGAGGTTGCAATG 60
DB 285 AGCCACTGGGAGGCTTAAATGGAGAAATCGCTGAACCTGAGGAGGAGGTTGCAATG 344
QY 61 AGCCGAGATCAAGGCTGAGACAGAGATCGTTGAACCCGGAGGAGAGGTTGCAATG 120
DB 345 AGCCGAGATCAAGGCTGAGACAGAGATCGTTGAACCCGGAGGAGAGGTTGCAATG 404
QY 121 AAAAAAAAAATCGTTACATTTATGTTGATT 152
DB 405 AAAAAAAAAAGTTAGAAAAATGCTGCTT 436

RESULT 10
LOCUS BU782096 584 bp mRNA linear EST 11-OCT-2002
DEFINITION

```

DEFINITION      1m99h05.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6123129
ACCESSION       BU782096
VERSION         BU782096.1 GI:23825019
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 584)
                Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                Lemschka,I., Sceaer,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                Hillier,L., Maria,M., Page,D., Wylie,T., Martin,J., Blistain,A.,
                Schmitt,A., Theising,B., Rifter,E., Ronko,I., Bennett,J.,
                Cardenas,M., Gibbons,M., McCan,R., Cole,R., Tsagarishvili,R.,
                Williams,T., Jackson,Y. and Bowers,Y.
                Endocrine Pancreas Consortium
                Unpublished (2000)
TITLE           Endocrine Pancreas Consortium
JOURNAL         Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                Endocrine Pancreas Consortium
                Harvard University, Howard Hughes Medical Institute
                Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                MA 02138
                Tel: 617-495-1812
                Fax: 617-495-8557
                Email: dmelton@biohp.harvard.edu
                Library was constructed by Dr. J. Ferrer In vivo mass-excised to
                pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
                University Genome Sequencing Center For information on obtaining a
                clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
                Seq primer: -40RP from Gibco
                High quality sequence scop: 426.
FEATURES        Location/Qualifiers
                source          1..584
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6123129"
                /tissue_type="Insulinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="Human Insulinoma"
                /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
                XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
                (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                pBluescript SK- by Dr. H. Inoue following the Washington
                University protocol
                (http://genome.wustl.edu/est/lambda_protocol.shtml).
                Please contact Hiroshi Inoue, MD/PhD for further
                information on this library (Metabolism Division, Permutt
                Laboratory, Washington University School of Medicine, Box
                8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                is a Washington University Pancreas EST project library."
ORIGIN
Query Match      12.4%; Score 107.2; DB 5; Length 584;
Best Local Similarity 81.6%; Pred. No. 4,6e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY 1 AGCTACTCAGAGGCTGAGACACGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60
DB 285 AGCCACTCGGAGGCTTAAATGGAGAAATCGTTGAACCTGAGGAGGAGGTTGCAGTG 344
OY 61 AGCCGAGATCAGCGCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCGA 120
DB 345 AGCCAGGACCAAGCGCACTGCACTCCATCCAGCCTGGGCTGACAGAGCAAGACTCCATCTCA 404
OY 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152
DB 405 AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

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RESULT 11
BQ270346

```

LOCUS           BQ270346      589 bp      mRNA      linear      EST 15-JUL-2003
DEFINITION      1k09g10.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5780562
ACCESSION       BQ270346
VERSION         BQ270346.1 GI:20495412
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 589)
                Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                Lemschka,I., Sceaer,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                Hillier,L., Maria,M., Page,D., Wylie,T., Martin,J., Blistain,A.,
                Schmitt,A., Theising,B., Rifter,E., Ronko,I., Bennett,J.,
                Cardenas,M., Gibbons,M., McCan,R., Cole,R., Tsagarishvili,R.,
                Williams,T., Jackson,Y. and Bowers,Y.
                Endocrine Pancreas Consortium
                Unpublished (2000)
TITLE           Endocrine Pancreas Consortium
JOURNAL         Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                Endocrine Pancreas Consortium
                Harvard University, Howard Hughes Medical Institute
                Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                MA 02138
                Tel: 617-495-1812
                Fax: 617-495-8557
                Email: dmelton@biohp.harvard.edu
                Library was constructed by Dr. J. Ferrer In vivo mass-excised to
                pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
                University Genome Sequencing Center For information on obtaining a
                clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
                Seq primer: -40RP from Gibco
                High quality sequence scop: 427.
FEATURES        Location/Qualifiers
                source          1..589
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5780562"
                /tissue_type="Insulinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="Human Insulinoma"
                /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
                XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
                (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                pBluescript SK- by Dr. H. Inoue following the Washington
                University protocol
                (http://genome.wustl.edu/est/lambda_protocol.shtml).
                Please contact Hiroshi Inoue, MD/PhD for further
                information on this library (Metabolism Division, Permutt
                Laboratory, Washington University School of Medicine, Box
                8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                is a Washington University Pancreas EST project library."
ORIGIN
Query Match      12.4%; Score 107.2; DB 5; Length 589;
Best Local Similarity 81.6%; Pred. No. 4,6e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY 1 AGCTACTCAGAGGCTGAGACACGAGAAATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60
DB 285 AGCCACTCGGAGGCTTAAATGGAGAAATCGTTGAACCTGAGGAGGAGGTTGCAGTG 344
OY 61 AGCCGAGATCAGCGCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCGA 120
DB 345 AGCCAGGACCAAGCGCACTGCACTCCATCCAGCCTGGGCTGACAGAGCAAGACTCCATCTCA 404
OY 121 AAAAAAAAAATCGTTACATTTATGCTGATT 152
DB 405 AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

```

RESULT 12

BU783590
 LOCUS BU783590 589 bp mRNA linear EST 11-OCT-2002
 DEFINITION in06e04.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6123727
 5', mRNA sequence.
 ACCESSION BU783590
 VERSION BU783590.1 GI:23827926
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
 Hillier, L., Scarsell, J., Gradow, J., Clifton, S.,
 Lemstra, I., Marra, M., Pape, D., Wylie, T., Martin, J., Bistrian, A.,
 Schmitt, A., Meising, B., Ritzer, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Other_ESTs: in06e04.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center for information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 428.
 Location/Qualifiers
 1..589
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6123727"
 /tissue_type="insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Human insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 xho1; Site_2: EcoRI; Constructed with lambda ZapIt system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permut
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas Est project library."

ORIGIN
 Query Match 12.4%; Score 107.2; DB 5; Length 589;
 Best Local Similarity 81.6%; Pred. No. 4.6e-16;
 Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

1 AGCTACTCAGAGGCTGAGACACGAAATCGCTTGAACCCGGAGGACGAGTTGCACG 60
 DB AGCCACTCGGAGGCTTAAATGGAGAAATCGCTTGAACCTTGAAGGACGAGTTGCACG 344
 285 AGCCACTCGGAGGCTTAAATGGAGAAATCGCTTGAACCTTGAAGGACGAGTTGCACG 344
 61 AGCCAGATCAGCGACCTGATCCATCCAGCTGGGCGAAGAGAGACGATCCGCTCA 120
 DB AGCCAGACGACGACCTGATCCATCCAGCTGGGCGAAGAGAGACGATCCGCTCA 404
 345 AGCCAGACGACGACCTGATCCATCCAGCTGGGCGAAGAGAGACGATCCGCTCA 404
 121 AAAAAAAAAAATGTTACATTTATGTTGATT 152
 DB AAAAAAAAAAATGTTACATTTATGTTGATT 436

RESULT 13
 LOCUS BX507946 564 bp mRNA linear EST 04-SEP-2003
 DEFINITION DKFZp686L09262.5, mRNA sequence.
 ACCESSION BX507946
 VERSION BX507946.1 GI:32043918
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
 Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fodor, G., Han, M. and
 Wiemann, S.
 TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,
 Wellenreuther, R., et al.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No 31 sequence available.
 This clone (DKFZp686L09262) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1..564
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686L09262"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="686 (synonym: hlc3)"
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
 Query Match 12.3%; Score 106.8; DB 5; Length 564;
 Best Local Similarity 82.0%; Pred. No. 5.7e-16;
 Matches 123; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

1 AGCTACTCAGAGGCTGAGACACGAAATCGCTTGAACCCGGAGGACGAGTTGCACG 60
 DB AGCTACTCAGAGGCTGAGACACGAAATCGCTTGAACCCGGAGGACGAGTTGCACG 221
 162 AGCTACTCAGAGGCTGAGACACGAAATCGCTTGAACCCGGAGGACGAGTTGCACG 221
 61 AGCCAGATCAGCGACCTGATCCATCCAGCTGGGCGAAGAGAGACGATCCGCTCA 120
 DB AGCCAGATCAGCGACCTGATCCATCCAGCTGGGCGAAGAGAGACGATCCGCTCA 281
 222 AGCCAGATCAGCGACCTGATCCATCCAGCTGGGCGAAGAGAGACGATCCGCTCA 281
 121 AAAAAAAAAAATGTTACATTTATGTTGGA 150
 DB AAAAAAAAAAATGTTACATTTATGTTGGA 311

RESULT 14
 LOCUS AQ428429 635 bp DNA linear GSS 24-MAR-1999
 DEFINITION CITBI-EL-2564J3, TF CITBI-EL Homo sapiens genomic clone 2564J3,
 genomic survey sequence.
 ACCESSION AQ428429
 VERSION AQ428429.1 GI:4496195
 GSS.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 635)

REFERENCE Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

AUTHORS Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other_GSSS: CITBI-E1-2564J3.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org

FEATURES Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html. Seq primer: M13-21
Classes: BAC ends.

source Location/Qualifiers
1..635
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2564J3"
/sex="male"
/cell_type="sperm"
/clone_1ib="CITBI-E1"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"

ORIGIN

Query Match 12.3%; Score 106.4; DB 8; Length 635;
Best Local Similarity 67.3%; Pred. No. 7.3e-16;
Matches 167; Conservative 0; Mismatches 76; Indels 5; Gaps 1;

1 AGCTACTGAGGAGGCTGAGACGAGAAATCGCTGAACCCGGAGGAGGAGGTTGCAGTG 60
|||||
307 AGCTATTGAGGAGGCTGAGGAGGAGAAATCCTTGAAACCCGGAGGAGGTTGCAGTG 366
|||||
61 AGCCGAGATCAGCGCACTAGATCCATCCAGCCTGGCGAAAGAGCAAGACTCCGCTCA 120
|||||
367 AGCCGAGATCGCGCACTGCACTCCATCCAGCCTGGCGAAGAGGAGACTCCAGCTCA 426
|||||
121 AAAAAAAAAAATCGTTACAT-----TTATGTGGATTACTCCCTCTTTTACTTCATCA 175
|||||
427 AAAAAAAAAAATCGTTACATTTTAACTGATTAACCTTACACCAAGTTGATCAGACAA 486
|||||
176 AGACACAGCACTACTTTAAAGCAAGTCAATGATTGAAAGCGCTTCTTCTTAATAA 235
|||||
487 ACTACAGAGGTAAAGTAACTTAATTATTAATTAACCAAGTATTAATTGATAAATA 546
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236 GCGAGATT 243
|||||
547 TAGACAGT 554
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RESULT 15 CA428584 679 bp mRNA linear EST 07-NOV-2002
LOCUS CA428584/c
DEFINITION UT-H-FEI-bez-1-08-0-UT g1 NCI CGAP_FEI Homo sapiens cDNA clone
ACCESSION CA428584
VERSION CA428584.1 GI:24791310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 679)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA sequence: 11-67, >MER47B#DNA/MER2 type (matched complement)
507-672, >Alu (matched complement)
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UT-H-FEI-bez-1-08-0-UT"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1ib="NCI CGAP FE1"
/note="Organ: Chondrosarcoma; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FE1 is a normalized cDNA library derived from a pool of mRNA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCTACGAGC. The cell lines were provided by Dr James Martin from the University of Iowa.
TAG TISSUE=human grade 2 chondrosarcoma cell line pool
TAG_1ib=UT-H-FEI
TAG_SEQ=CGCTACGAGC"

ORIGIN

Query Match 12.2%; Score 106; DB 6; Length 679;
Best Local Similarity 84.9%; Pred. No. 9.2e-16;
Matches 118; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

1 AGCTACTGAGAGGCTGAGACGAGAAATCGCTGAACCCGGAGGAGGAGGTTGCAGTG 60
|||||
633 AGCCACTGAGAGGCTTAAATGGGAATCACTTAACCCCTGGAGGAGGTTGCAGTG 574
|||||
61 AGCCGAGATCAGCGCACTAGATCCATCCAGCCTGGCGAAAGAGCAAGACTCCGCTCA 120
|||||
573 AGCCGAGACAGCGCACTGCACTCCATCCAGCCTGGCGAAGAGCAAGACTCCATCTCA 514
|||||
121 AAAAAAAAAAATCGTTACAA 139
|||||
513 AAAAAAAAAAAGTTAGAA 495
|||||

Search completed: April 26, 2005, 20:13:32
Job time : 3696.27 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 15:59:17 ; Search time 595.011 Seconds
(without alignments)
8625.744 Million cell updates/sec

Title: US-09-601-267-36

Sequence: 1 agctactcgaagagctcgtaga.....ccctactcgaagagcgtga 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Listing first 45 summaries

Database:

1:	N_Geneseq_16Dec04:*
2:	geneseqn1980s:*
3:	geneseqn1990s:*
4:	geneseqn2000s:*
5:	geneseqn2001as:*
6:	geneseqn2001bs:*
7:	geneseqn2002as:*
8:	geneseqn2002bs:*
9:	geneseqn2003as:*
10:	geneseqn2003bs:*
11:	geneseqn2003ds:*
12:	geneseqn2004as:*
13:	geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	867	100.0	867	2	AAZ07250	Aaz07250 Human tel
2	867	100.0	1765	2	AAZ07247	Aaz07247 Human tel
3	848.6	97.9	2426	2	AAV22994	Aav22994 DNA contra
4	848.6	97.9	2426	10	ADC21254	Adc21254 Plasmid P
5	834.6	96.3	2425	2	AAT11027	Aat11027 DNA encod
6	834.6	96.3	2425	2	AAT10283	Aat10283 Gene for
7	334	38.5	981	2	AAV41194	Aav41194 Pcti frag
8	334	38.5	981	2	AAV19481	Aav19481 Human tel
9	333	38.4	980	4	AA509471	AA509471 Human DNA
10	333	38.4	981	6	AAAD4234	AAad4234 Human tel
11	332.4	38.3	981	2	AAAT9242	AAat8242 Clone con
12	332.4	38.3	981	2	AAV63644	AAv63644 Human tel
13	332.4	38.3	981	2	AAZ23626	AAz23626 Human clo
14	332.4	38.3	981	3	AAAT37564	AAa37564 Human tel
15	332.4	38.3	981	4	AAAT5442	AAa5442 Pcti frag
16	285	32.9	966	12	ADG82572	Adg82572 Human tel
17	176	20.3	176	2	AAZ07323	Aaz07323 Human tel
18	176	20.3	176	2	AAZ07251	Aaz07251 Human tel
19	163	18.8	545	8	ACC57551	Acc57551 Human tel
20	163	18.8	545	10	ACC58040	Acc58040 Human tel

21	155	17.9	680	2	AAT58803	Aat58803 Human tel
22	110.8	12.8	340449	8	AAI52198	Aai52198 Human sec
23	109.4	12.6	110060	12	ADQ97050_0	Adq97050 Human can
24	109.2	12.6	133893	9	AAAD5438	AAad5438 Human pho
25	108.6	12.5	76698	12	ADU84182	Adu84182 Human c-r
26	107	12.3	178024	12	ADQ97721	Adq97721 Human can
27	106.4	12.3	86764	12	ADQ97623	Adq97623 Human can
28	106.2	12.2	2275	10	ADG62229	Adg62229 Human can
29	106.2	12.2	313287	13	ABD33100	Abd33100 Human can
30	106	12.2	15650	5	ABA16364	Abai6364 Human ner
31	106	12.2	15650	5	ABA15903	Abai5903 Human ner
32	106	12.2	42738	4	AAK68992	Aak68992 Human imm
33	106	12.2	138837	13	ABD33163	Abd33163 Human can
34	104.8	12.1	2133	11	ADM01783	Adm01783 Human can
35	104.8	12.1	26928	5	ABA82620	Abas82620 Human can
36	104.8	12.1	26928	6	ABK22779	Abk22779 Human hlg
37	104.8	12.1	26928	8	ACC45361	Acc45361 Human hlg
38	104.8	12.1	26928	10	ADB88061	Adb88061 HBM-relat
39	104.8	12.1	26928	10	ADB82430	Adb82430 Human DNA
40	104.8	12.1	26928	13	ADR16924	Adr16924 BAC clone
41	104.8	12.1	156843	11	ACN44786	Acn44786 Human gen
42	104.8	12.1	156843	11	ACN44786	Acn44786 Human gen
43	104.4	12.0	17570	8	ABZ74059	Abz74059 Secreted
44	104.4	12.0	17570	8	ADA98657	Ada98657 Human sec
45	104.4	12.0	17570	10	ABZ67655	Abz67655 Human sec

ALIGNMENTS

RESULT 1	AAZ07250	standard; DNA; 867 BP.
XX	AAZ07250:	
XX	22-OCT-1999 (first entry)	
XX	Human telomerase RNA gene (HTR) 5' flanking region.	
XX	Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;	
KW	Gene therapy; thymidine kinase gene; anticancer therapy; human; ss.	
OS	Homo sapiens.	
XX	WO938964-A2.	
XX	05-AUG-1999.	
XX	29-JAN-1999; 99WO-GB000308.	
XX	29-JAN-1998; 98GB-00001902.	
XX	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.	
XX	Keith MN;	
XX	WPI; 1999-479183/40.	
XX	Mouse and human telomerase RNA gene promoters, useful for tumor specific gene therapy.	
XX	Claim 3; Fig 4a; 10ppp; English.	
XX	The invention relates to promoter regions from mouse and human telomerase RNA (TR) component genes. The TR gene promoter can be linked to a heterologous gene, especially a gene encoding a cytotoxin, for therapy of cancer, especially neoplasias. The telomerase is necessary for the unrestricted proliferative capacity of many human cancers. Mutation or dysregulation of the telomerase repression pathway may cause reactivation or upregulation of the telomerase expression in cancer. Substances, identified in the methods, can be used to block transcription from the TR gene promoter through interaction of the 5' regulatory sequences. These	

CC substances, e.g. antisense oligonucleotides, transcription factors,
 CC peptide nucleic acids and factors that disrupt signal transduction, are
 CC useful for cancer therapy. In particular, gene therapy vectors
 CC (especially pG62-codapp) comprising the promoter and a viral thymidine
 CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
 CC neoplasia can be controlled or treated. Direct down-regulation of
 CC telomerase RNA gene through manipulation of transcription factors may be
 CC effective anticancer therapy and the cloning of the hTR gene promoter
 CC allows the analysis of therapeutic molecules which modulate hTR promoter
 CC activity. The present sequence represents a human TR gene (hTR) 5'
 CC flanking sequence

XX
 XX Sequence 867 BP; 237 A; 209 C; 221 G; 200 T; 0 U; 0 Other;

Query Match 100.0%; Score 867; DB 2; Length 867;
 Best Local Similarity 100.0%; Pred. No. 1,4e-267;

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACAGAAATCGCTTGAACCGGGGAGCAGAGGTTGACAGT 60
 DB 1 AGCTACTCAGAGGCTGAGACAGAAATCGCTTGAACCGGGGAGCAGAGGTTGACAGT 60
 QY 61 AGCCGAGATCAGCCGCACTAGACTCCATCCAGCTGGCGAAGAGCAAGATCCGCTCTCA 120
 DB 61 AGCCGAGATCAGCCGCACTAGACTCCATCCAGCTGGCGAAGAGCAAGATCCGCTCTCA 120
 QY 121 AAAAAAAAAATCGTTACATTTTATGATGATTAATCTCCCTCTTTTAACTCATCAAGACA 180
 DB 121 AAAAAAAAAATCGTTACATTTTATGATGATTAATCTCCCTCTTTTAACTCATCAAGACA 180
 QY 181 CAGCACTACTTTAAGCAAGTCAATGATGAAGAGCTTCTTCTTAAATAAAGGAG 240
 DB 181 CAGCACTACTTTAAGCAAGTCAATGATGAAGAGCTTCTTCTTAAATAAAGGAG 240
 QY 241 ATTCACTCTTAAGATTAATTAATGATGATTAATCACTTGAATTAAGCATCTCTGCTCA 300
 DB 241 ATTCACTCTTAAGATTAATTAATGATGATTAATCACTTGAATTAAGCATCTCTGCTCA 300
 QY 301 AGGAGAAGCTGGAGAGGCAATCTTAAGAGAAAGGGGAGGTTGAACTCGGACGATC 360
 DB 301 AGGAGAAGCTGGAGAGGCAATCTTAAGAGAAAGGGGAGGTTGAACTCGGACGATC 360
 QY 361 CCACTGAGCCGAGACAGATTTCTGCTAGTCAAGTGCCTGGAAATCTATTTTACA 420
 DB 361 CCACTGAGCCGAGACAGATTTCTGCTAGTCAAGTGCCTGGAAATCTATTTTACA 420
 QY 421 AGTTCTCCAAAAATGATGATCAAACTAGGAATTAATGTTCTGTCTTAAAGCCCTTA 480
 DB 421 AGTTCTCCAAAAATGATGATCAAACTAGGAATTAATGTTCTGTCTTAAAGCCCTTA 480
 QY 481 AAATCTCTCTGTAATTCATTTTAAAGTGAAGTGAACCGGGTCTGCTGACGA 540
 DB 481 AAATCTCTCTGTAATTCATTTTAAAGTGAAGTGAACCGGGTCTGCTGACGA 540
 QY 541 GGATGAAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTCCGAG 600
 DB 541 GGATGAAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTCCGAG 600
 QY 601 TAAAGACGAAAGCTTTCCCGGAGCGTGGGAGAGGCAAGTCTTCTCATAGCCGGA 660
 DB 601 TAAAGACGAAAGCTTTCCCGGAGCGTGGGAGAGGCAAGTCTTCTCATAGCCGGA 660
 QY 661 ATGGAATTTAATTTCCCGTTCCCGCAACAGCCGCGGAGAGAGTGAATCTGACGAG 720
 DB 661 ATGGAATTTAATTTCCCGTTCCCGCAACAGCCGCGGAGAGAGTGAATCTGACGAG 720
 QY 721 AGCCGAGAGTCAAGTCTGGCCCAATCGGCTCGGCGGCGCTCCCTTAAAGCCGA 780
 DB 721 AGCCGAGAGTCAAGTCTGGCCCAATCGGCTCGGCGGCGCTCCCTTAAAGCCGA 780
 QY 781 CTCGCCCCGAGCGACCCGGGTTGCGAGAGGTGGGCTCGGAGAGGTGGGCAATTTT 840
 DB 781 CTCGCCCCGAGCGACCCGGGTTGCGAGAGGTGGGCTCGGAGAGGTGGGCAATTTT 840

QY 841 TGTCTAACCTTAACCTGAGAGAGGCGCTGA 867
 DB 841 TGTCTAACCTTAACCTGAGAGAGGCGCTGA 867

RESULT 2

AAZ07247
 ID AAZ07247 standard; DNA; 1765 BP.

XX AAZ07247;

AC 22-OCT-1999 (first entry)

XX Human telomerase RNA (hTR) gene sequence.

XX Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
 KM gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

XX Homo sapiens.

PN MO938964-A2.

PD 05-AUG-1999.

PF 29-JUN-1999; 99WO-GB000308.

PR 29-JUN-1998; 98GB-00001902.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

PI Keith W.

DR WPI; 1999-479183/40.

PT Mouse and human telomerase RNA gene promoters, useful for tumor specific
 gene therapy.

XX
 XX
 PS Disclosure; Fig 1; 109pp; English.

CC The invention relates to promoter regions from mouse and human telomerase
 CC RNA (TR) component genes. The TR gene promoter can be linked to a
 CC heterologous gene, especially a gene encoding a cytotoxin, for therapy of
 CC cancer, especially neoplasias. The telomerase is necessary for the
 CC unrestricted proliferative capacity of many human cancers. Mutation or
 CC dysregulation of the telomerase repression pathway may cause reactivation
 CC or upregulation of telomerase expression in cancer. Substances,
 CC identified in the methods, can be used to block transcription from the TR
 CC gene promoter through interaction of the 5' regulatory sequences. These
 CC substances, e.g. antisense oligonucleotides, transcription factors,
 CC peptide nucleic acids and factors that disrupt signal transduction, are
 CC useful for cancer therapy. In particular, gene therapy vectors
 CC (especially pG62-codapp) comprising the promoter and a viral thymidine
 CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
 CC neoplasia can be controlled or treated. Direct down-regulation of
 CC telomerase RNA gene through manipulation of transcription factors may be
 CC effective anticancer therapy and the cloning of the hTR gene promoter
 CC allows the analysis of therapeutic molecules which modulate hTR promoter
 CC activity. The present sequence represents a human TR gene sequence

XX
 XX Sequence 1765 BP; 404 A; 458 C; 480 G; 423 T; 0 U; 0 Other;

Query Match 100.0%; Score 867; DB 2; Length 1765;

Best Local Similarity 100.0%; Pred. No. 2.1e-267;

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTACTCAGAGGCTGAGACAGAAATCGCTTGAACCCGGGAGCAGAGGTTGACAGT 60
 DB 1 AACTACTCAGAGGCTGAGACAGAAATCGCTTGAACCCGGGAGCAGAGGTTGACAGT 60
 QY 61 ACCCGAGATCAGCCCACTAGACTCCATCCAGCTGGGAGAAAGACCAAGATCCGCTCTCA 120
 DB 61 ACCCGAGATCAGCCCACTAGACTCCATCCAGCTGGGAGAAAGACCAAGATCCGCTCTCA 120

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QY 121 AAAAAAAAAATCGTCAATTATGNGATTAATCCCTCTTTTACTCATCAAGACA 180
DB 121 AAAAAAAAAATCGTCAATTATGNGATTAATCCCTCTTTTACTCATCAAGACA 180
QY 181 CAGCACTACTTTAAGCAAGTCAATGATGAAACGCTTCTTCTTAATAAAGGAG 240
DB 181 CAGCACTACTTTAAGCAAGTCAATGATGAAACGCTTCTTCTTAATAAAGGAG 240
QY 241 ATTCACTCTTAAGATTAATATGATGATTAACCTTGAATTAAGCCATCTCTGCTCA 300
DB 241 ATTCACTCTTAAGATTAATATGATGATTAACCTTGAATTAAGCCATCTCTGCTCA 300
QY 301 AGGAGAGCTGGGAGGAGGATCTTAAGGAAAAGGGGCGGGTGGAACTCGGAGCCATC 360
DB 301 AGGAGAGCTGGGAGGAGGATCTTAAGGAAAAGGGGCGGGTGGAACTCGGAGCCATC 360
QY 361 CCACTGAGCGGAGACAAGATCTGCTGTAGTCAAGTCTGCTGGAACTATTTTCAAA 420
DB 361 CCACTGAGCGGAGACAAGATCTGCTGTAGTCAAGTCTGCTGGAACTATTTTCAAA 420
QY 421 AGTTCTCAAAAAATGTGATGATCAAACTAGGAATTAAGTGTCTGTCTTAAGCCCTTA 480
DB 421 AGTTCTCAAAAAATGTGATGATCAAACTAGGAATTAAGTGTCTGTCTTAAGCCCTTA 480
QY 481 AATCTCTCTGTAATTCATTTTAAAGGATGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 AATCTCTCTGTAATTCATTTTAAAGGATGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGATGAAAAAAGGCGCTCTGATACCTCAAGTATGTTTCACTTAAAGAGGTCGGAAG 600
DB 541 GGATGAAAAAAGGCGCTCTGATACCTCAAGTATGTTTCACTTAAAGAGGTCGGAAG 600
QY 601 TAAAGACGAAAGCTTTTCCCGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 TAAAGACGAAAGCTTTTCCCGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 ATGGAACCTTAATTTCCCTCCCGCAACCGCCGCGGAGAGGATCACTTCACGAG 720
DB 661 ATGGAACCTTAATTTCCCTCCCGCAACCGCCGCGGAGAGGATCACTTCACGAG 720
QY 721 ACCCGGAGAGTCAAGTTCGCAATCCGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 ACCCGGAGAGTCAAGTTCGCAATCCGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 CTGCGCCGCGCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 CTGCGCCGCGCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 TGTCTAACCTTAACCTGAAGAAAGGCGGTA 867
DB 841 TGTCTAACCTTAACCTGAAGAAAGGCGGTA 867

```

RESULT 3
AAV22994 standard; DNA; 2426 BP.
AAV22994;

30-JUL-1998 (first entry)
DNA containing human telomerase RNA component gene sequences.
Human; telomerase RNA component gene sequence; ribonucleoprotein enzyme;
cancer cell; telomerase activity; reporter construct;
transcription regulatory region; prophylaxis; therapy;
telomerase-related condition; chromatin position effect; ss.
Homo sapiens.
Key Location/Qualifiers
FT misc_feature 1234..1245

```

FT FT /*tag= f
FT FT /note= "beta-interferon response element"
FT FT misc_feature 1238..1259
FT FT /*tag= b
FT FT /note= "PSE consensus sequence"
FT FT misc_feature 1354..1359
FT FT /*tag= e
FT FT /note= "SP1 consensus sequence"
FT FT CAAAT_signal 1399..1406
FT FT /*tag= d
FT FT misc_feature 1406..1414
FT FT /*tag= c
FT FT /note= "PSE consensus sequence"
FT FT TATA_signal 1438..1444
FT FT /*tag= a
FT FT MO9811207-A2.
FT FT 19-MAR-1998.
FT FT 16-SEP-1997; 97WO-US016450.
FT FT 16-SEP-1996; 96US-00714482.
FT FT (GERO-) GERON CORP.
FT FT Villeponteau B. Harley C;
FT FT WPI; 1998-207376/18.
FT FT Human telomerase reporter constructs - useful in assays for regulators of
FT FT mammalian telomerase expression.
FT FT Claim 6; Page 27-28; 59pp; English.
FT FT
FT FT The present sequence contains human telomerase RNA component gene
FT FT sequences. Telomerase is a ribonucleoprotein enzyme that synthesizes one
FT FT strand of the telomeric DNA using as a template a sequence contained
FT FT within the RNA component of the enzyme. Most cancer cells express high
FT FT levels of telomerase activity, while in normal somatic human cells,
FT FT telomerase is not detected. The specification describes the production of
FT FT a telomerase reporter construct which comprises a recombinant
FT FT polynucleotide having a transcription regulatory region of a telomerase
FT FT gene operably linked to a nucleotide sequence encoding a reporter
FT FT polynucleotide heterologous to the transcription regulatory region.
FT FT Expression of the reporter polynucleotide is detectable. The telomerase
FT FT reporter construct is used in screening assays for determining modulators
FT FT of transcription. The modulators can be used for prophylaxis or therapy
FT FT of telomerase-related conditions. The reporter construct which has a
FT FT selectable drug marker can be used to generate position effect reporter
FT FT cells which can be used to determine whether a test agent inhibits
FT FT chromatin position effect. Tagged RNA component constructs can be used to
FT FT determine whether an agent modulates association between a mammalian RNA
FT FT telomerase component and a mammalian telomerase
FT FT
FT FT Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 U; 0 Other;
FT FT
FT FT Query Match 97.9%; Score 848.6; DB 2; Length 2426;
FT FT Best Local Similarity 99.4%; Pred. No. 2.1e-261;
FT FT Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

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QY 1 ACCTACTCAGAGGCGTGGAGACACGAGATCGCTTGAACCCGGGAGGAGGAGGAGGAGGAGG 60
DB 662 ACCTACTCAGAGGCGTGGAGACACGAGATCGCTTGAACCCGGGAGGAGGAGGAGGAGGAGG 720
QY 61 ACCCGAGATCAAGCACTAGACTCCATCCAGCTGCGGCGAAGAGACAGACTCCGCTCA 120
DB 721 ACCCGAGATCAAGCACTAGACTCCATCCAGCTGCGGCGAAGAGACAGACTCCGCTCA 780
QY 121 AAAAAAAAAATCGTCAATTATGNGATTAATCCCTCTTTTACTCATCAAGACA 180
DB 781 AAAAAAAAAATCGTCAATTATGNGATTAATCCCTCTTTTACTCATCAAGACA 840

```

OY		181	CAGCAGCTACTTTAAAGCAAGTCANGTGGAACGCCCTTCTTCCATTAAGAAGG	240
Dd		841	CAGCATCTATTAAAGCAAGTCANGTGGAACGCCCTTCTTCCATTAAGAAGG	900
OY		241	ATTGAGTCTTAAAGATTATAATATGATAGTATCACTTGATTAAGCATCCTCGTCA	300
Dd		901	ATTGAGTCTTAAAGATTATAATATGATAGTATCACTTGATTAAGCATCCTCGTCA	960
OY		301	AGGAAAGCTGGAGAAAGGCATTTCTAAGAAAAAGGGGCAAGGTTTGGAACTCGACGCATC	360
Dd		961	AGGAAAGCTGGAGAAAGGCATTTCTAAGAAAAAGGGGCAAGGTTTGGAACTCGACGCATC	1020
OY		361	CCACTGAGCCGAGACAAGATTCGCTGATGTCAGTGCCTGCGGAAATCTATTTTCAAA	420
Dd		1021	CCACTGAGCCGAGACAAGATTCGCTGATGTCAGTGCCTGCGGAAATCTATTTTCAAA	1080
OY		421	AGTTCTCCAAAANAATGTGATGATCAAAAATAGAAATTAGTGTCTGTCTTAAGCCCTA	480
Dd		1081	AGTTCTCCAAAANAATGTGATGATCAAAAATAGAAATTAGTGTCTGTCTTAAGCCCTA	1140
OY		481	AAATCTTCTGTGAATTCATTTTTAAGTAGTGTGAGGTTGAACCGCGCTGCTGCAGAA	540
Dd		1141	AAATCTTCTGTGAATTCATTTTTAAGTAGTGTGAGGTTGAACCGCGCTGCTGCAGAA	1200
OY		541	GGAATGAAAAAAGGCTCTGTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTCGAAAG	600
Dd		1201	GGAATGAAAAAAGGCTCTGTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTCGAAAG	1260
OY		601	TAAAGACCCAAAAGCCTTTCCCGGACATGTCGGAAGGGCAAAGTCTTCTCTATAGCCGGA	660
Dd		1261	TAAAGACCCAAAAGCCTTTCCCGGACATGTCGGAAGGGCAAAGTCTTCTCTATAGCCGGA	1320
OY		661	ATGGAATCTTAATTTCCCGGTTCCCGCCCAACAGACCGGCGCAGAGAGTGACTTCAAGAG	720
Dd		1321	ATGGAATCTTAATTTCCCGGTTCCCGCCCAACAGACCGGCGCAGAGAGTGACTTCAAGAG	1380
OY		721	AGCCGCGAGATCAAGCTTGCGCAATCCGTGCGGTGCGCGCCGCTCCCTTTATAAGCCGA	780
Dd		1381	AGCCGCGAGATCAAGCTTGCGCAATCCGTGCGGTGCGCGCCGCTCCCTTTATAAGCCGA	1440
OY		781	CTCCGCCGCGAGCGCACCGGGTTGCGAGGGGCTGCGGAGGGGGTGTGGCAATTTT	840
Dd		1441	CTCCGCCGCGAGCGCACCGGGTTGCGAGGGGCTGCGGAGGGGGTGTGGCAATTTT	1500
OY		841	TGTTCTAACCTTAACCTGAGAGAGGCGTGA	867
Dd		1501	TGTTCTAACCTTAACCTGAGAGAGGCGTGA	1527
<hr/>				
RESULT 4				
ID	ADC21254			
AD	ADC21254 standard; DNA; 2426 BP.			
XX	ADC21254;			
AC	18-DEC-2003 (first entry)			
DT				
XX				
DE	Plasmid pGRN3 insert containing human TR DNA.			
XX				
KW	Viral vector; heterologous control element; gene expression;			
KM	human telomerase reverse transcriptase; hTERT; tumour specific gene;			
KW	cell death; transcriptional control element;			
KM	human telomerase RNA component; hTR; cancer cell; liver cancer;			
KW	prostate cancer; muscle cancer; neutral cell cancer; lung cancer;			
KM	osteosarcoma; medulloblastoma; cervical carcinoma; fibrosarcoma;			
KW	osteosarcoma; plasmid pGRN33; human; ds.			
XX				
OS	Synthetic.			
OS	Homo sapiens.			
PN	US2003099616-A1.			
XX				
DD	29-MAY-2003.			

XX	25-JUL-2002; 2002US-00206447.
XX	PF
XX	PR 25-JUL-2001; 2001US-0308029P.
XX	PA (IRVI/) IRVING J M.
XX	PA (KARP) KARP D B.
XX	PA (SCHI/) SCHIFF J M.
XX	PI Irving JM, Karpf DB, Schiff JM;
XX	DR WPI; 2003-730140/69.
PT	New dual specificity vectors driven by the telomerase promoter, useful
PT	for killing or slowing the growth of tumor cells, or for treating cancer,
PT	e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
XX	
PS	Example 5; Page 20-21; 25pp; English.
CC	The present invention relates to a viral vector comprising first and
CC	second genes controlled by heterologous control elements, where the first
CC	gene is preferentially expressed in cells expressing human telomerase
CC	reverse transcriptase (hTERT), and another gene under the control of a
CC	heterologous transcriptional control element for a tissue or tumour
CC	specific gene other than TERT, and where transduction of the vector into
CC	a mammalian cell expressing TERT causes the death of the cell or its
CC	progeny. In particular, the second gene may be under the control of a
CC	transcriptional control element for a tissue specific gene selected from
CC	albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial
CC	creatine kinase, myelin basic protein, glial fibrillary acidic protein,
CC	and neuron-specific enolase. The second gene may be under the control of
CC	a transcriptional control element for a human telomerase RNA component
CC	(hTR). The vector of the invention is useful for killing a cancer cell,
CC	or treating a subject for a condition associated with increased
CC	expression of TERT in affected cells. The vector is also useful in the
CC	preparation of a medicament for treatment of a condition associated with
CC	increased expression of TERT, particularly cancer, and especially liver
CC	cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,
CC	pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and
CC	osteosarcoma. The present sequence represents plasmid pGRN33 insert
CC	containing human TR DNA.
SQ	Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 U; 0 Other;
	Query Match 97.9%; Score 848.6; DB 10; Length 2426;
	Best Local Similarity 99.4%; Pred. No. 2.1e-261;
	Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1
DY	1 AGCTACTCAGGAGGTGGAGACACGAAATCGCTTGAAACC GGGAAGGTCAGTG 60
Db	662 AGCTACTCAGGAGGTGGAGACACGAAATCGCTTGAAACC GGGA-GCGAAGGTTCAGTG 720
DY	61 AGCGGAGTCACGCCCATAGACATCACCTCAGCTGGGGGAAAGAACAAGATCCGCTCA 120
Db	721 AGCGGAGTCACGCCCATAGACATCACCTCAGCTGGGGGAAAGAACAAGATCCGCTCA 780
DY	121 AAAAAAAAAATCGTTACATTATGTGGATTAAGTACTCCCTCTTTTACCTCATCAAGACA 180
Db	781 AAAAAAAAAATCGTTACATTATGTGGATTAAGTACTCCCTCTTTTACCTCATCAAGACA 840
DY	181 CAGACATCTTTAAGCAAGTCAATATGAACGCCTTCTTCTTAATAAANGAG 240
Db	841 CAGACATCTTTAAGCAAGTCAATATGAACGCCTTCTTCTTAATAAANGAG 900
DY	241 ATTCACTCTTTAAGATTATATATGTAGTTACACTTGAATTAAGCATCTCTGTCTCA 300
Db	901 ATTCACTCTTTAAGATTATATATGTAGTTACACTTGAATTAAGCATCTCTGTCTCA 960
DY	301 AGGAGAGCTGTGAGAACGCATTTCAAGAAAAAGGGGCTGGAACTGGAGCATC 360
Db	961 AGGAGAGCTGTGAGAACGCATTTCTAAGAGAAAGGGGCTGGAACTGGAGCATC 1020
DY	361 CCACTGAGCGGAGCAAGATTCTGCTGATCACTGCTGCTGGGAAATCTATTTTCAAA 420

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DB 1021 CCACTAGCGGAGACAAAGATTCGTGTAGTCAGTGTGCTGGAAATCATTTTACAA 1080
QY 421 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTTAGTGTCTGTCTTAGGCCCTTA 480
DB 1081 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTTAGTGTCTGTCTTAGGCCCTTA 1140
QY 481 AAATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGGCTGTCTGCTGACAA 540
DB 1141 AAATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGGCTGTCTGCTGACAA 1200
QY 541 GGATGAAAAAAGGCGCTCTGATACCTCAAGTAGTTTCACTTTAAAGAGTCCGAAG 600
DB 1201 GGATGAAAAAAGGCGCTCTGATACCTCAAGTAGTTTCACTTTAAAGAGTCCGAAG 1260
QY 601 TAAAGACGAAAGCCTTTCCCGAGCTGCGAAGGCGCAACGTCCTTCTCATGCGCGAA 660
DB 1261 TAAAGACGAAAGCCTTTCCCGAGCTGCGAAGGCGCAACGTCCTTCTCATGCGCGAA 1320
QY 661 ATGGAACCTTAATTTCCGTTCCCGCAACGCGCGCGAGAGTGAATCTCTCAAG 720
DB 1321 ATGGAACCTTAATTTCCGTTCCCGCAACGCGCGCGAGAGTGAATCTCTCAAG 1380
QY 721 AGCCGCGAGAGTCAAGCTTGGCCAAATCCGTGCGGCGCGCTCCCTTTAAAGCCGA 780
DB 1381 AGCCGCGAGAGTCAAGCTTGGCCAAATCCGTGCGGCGCGCTCCCTTTAAAGCCGA 1440
QY 781 CTCGCCGCGACGCAACCGGCTTGGCGAGGGTGGGCTTGGAGAGGGTGGGCAATTTT 840
DB 1441 CTCGCCGCGACGCAACCGGCTTGGCGAGGGTGGGCTTGGAGAGGGTGGGCAATTTT 1500
QY 841 TGTCTTAACCTTAACCTGAAGAGGCGCTA 867
DB 1501 TGTCTTAACCTTAACCTGAAGAGGCGCTA 1527

RESULT 5
AAT11027
ID AAT11027 standard; DNA; 2425 BP.
XX
AC AAT11027;
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the human telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
XX probe; primer; ribozyme; ss.
XX
OS Homo sapiens.
XX
PN W09601614-A2.
XX
PD 25-JAN-1996.
XX
PE 07-JUL-1995; 95WO-US008620.
XX
PR 07-JUL-1994; 94US-00272102.
XX 27-OCT-1994; 94US-0030123.
XX 13-FEB-1995; 95US-00387524.
XX 07-JUN-1995; 95US-00485778.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C, Marhenda NA,
XX Villeponteau B;
XX
DR WPI; 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in studying
XX cell renaissance and immortalisation.

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PS Claim 37; Fig 1; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially from
CC mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the telomerase;
CC probes and primers can be used in detection; vectors and host cells
CC transformed with the isolated telomerase genes can be used for production
CC of telomerase; RNA and DNA ribozymes and triplex forming
CC oligonucleotides directed against the telomerase genes can be used
CC therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC (also claimed) can be used for study of telomere regulation in vivo, and
CC the role it plays in immortalisation. This DNA sequence encodes the human
CC telomerase RNA component
SQ
Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 U; 0 Other;
Query Match 96.3%; Score 834.6; DB 2; Length 2425;
Best Local Similarity 99.0%; Pred. No. 6; 7e-257;
Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;
QY 1 AGCTACTCGAGAGGCTGAGACACGAAATCGTTGAACCCGGAGGCAAGGTTGACATG 60
DB 662 AGCTACTCGAGAGGCTGAGACACGAAATCGTTGAACCCGGAGGCAAGGTTGACATG 720
QY 61 AGCCGAGATCAGCCACTGACATCCAGGCTGGGCGAAGAGCAAGACTCCGTTCA 120
DB 721 AGCCGAGATCAGCCACTGACATCCAGGCTGGGCGAAGAGCAAGACTCCGTTCA 780
QY 121 AAAAAAAAAAATGTTAACTTTAATTTAGTGAATTTACTCCCTCTTTTAACTCATCAAGACA 180
DB 781 AAAAAAAAAAATGTTAACTTTAATTTAGTGAATTTACTCCCTCTTTTAACTCATCAAGACA 840
QY 181 CAGCACTACTTTAAAGCAAGTCAATGATGAAGGCTTTCTTTCTTAATAAAGGGAG 240
DB 841 CAGCACTACTTTAAAGCAAGTCAATGATGAAGGCTTTCTTTCTTAATAAAGGGAG 900
QY 241 ATTCACTCTTAAGATTAATATGATAGTATGATCACTGATTAAGGCAATCCCTGTGCTCA 300
DB 901 ATTCACTCTTAAGATTAATATGATAGTATGATCACTGATTAAGGCAATCCCTGTGCTCA 960
QY 301 AGGAGAGCTGAGAGGAGGATTTCTAAGAAAAAGGGGCAAGGTTGGAACTCGAGCGCATC 360
DB 961 AGGAGAGCTGAGAGGAGGATTTCTAAGAAAAAGGGGCAAGGTTGGAACTCGAGCGCATC 1020
QY 361 CCACTGAGCCGAGACAAAGTTCTGCTGTAGTCAAGTCCCTGGGAAATCTATTTTACAA 420
DB 1021 CCACTGAGCCGAGACAAAGTTCTGCTGTAGTCAAGTCCCTGGGAAATCTATTTTACAA 1080
QY 421 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTTAGTGTCTGTCTTAGGCCCTTA 480
DB 1081 AGTTCTCCAAAAATGTGATGATCAAAACTAGAAATTTAGTGTCTGTCTTAGGCCCTTA 1140
QY 481 AAATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGGCTGTCTGCTGACAA 540
DB 1141 AAATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGGCTGTCTGCTGACAA 1200
QY 541 GGATGAAAAAAGGCGCTCTGATACCTCAAGTAGTTTCACTTTAAAGAGTCCGAAG 600
DB 1201 GGATGAAAAAAGGCGCTCTGATACCTCAAGTAGTTTCACTTTAAAGAGTCCGAAG 1260
QY 601 TAAAGACGAAAGCCTTTCCCGAGCTGCGAAGGCGCAACGTCCTTCTCATGCGCGAA 660
DB 1261 TAAAGACGAAAGCCTTTCCCGAGCTGCGAAGGCGCAACGTCCTTCTCATGCGCGAA 1320
QY 661 ATGGAACCTTAATTTCCGTTCCCGCAACGCGCGCGAGAGTGAATCTCTCAAG 720
DB 1321 ATGGAACCTTAATTTCCGTTCCCGCAACGCGCGCGAGAGTGAATCTCTCAAG 1380
QY 721 AGCCGCGAGAGTCAAGCTTGGCCAAATCCGTGCGGCGCGCTCCCTTTAAAGCCGA 780
DB 1381 AGCCGCGAGAGTCAAGCTTGGCCAAATCCGTGCGGCGCGCTCCCTTTAAAGCCGA 1440
QY 781 CTCGCCGCGACGCAACCGGCTTGGCGAGGGTGGGCTTGGAGAGGGTGGGCAATTTT 836

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Db 1441 CTCGCCGCGGACCGGCTTCCGAGAGGAGGCTGGAGGAGGCTGAT 1500
 QY 837 TTTTGTCTAACCTTAACCTGAGAAAGGCGTA 867
 Db 1501 TTTTGTCTAACCTTAACCTGAGAAAGGCGTA 1531

RESULT 6

AA110283
 ID AA110283 standard; DNA; 2425 BP.

AC AA110283;

XX 09-SEP-1996 (first entry)

DE Gene for RNA component of human telomerase.

XX RNA component; human; telomerase; lung fibroblast; cell line WI-38;

KM recombinant production; synthesis; mutant; detection; mammalian;

KM identification; modulating agent; neoplastic condition; gene;

XX transcripional regulatory sequence; gene therapy; disease; ss.

OS Homo sapiens.

XX MO9601835-A1.

XX 25-JAN-1996.

PF 06-JUL-1995; 95MO-US008530.

XX 07-JUL-1994; 94US-00272102.

PR 27-OCT-1994; 94US-00330123.

PR 07-JUN-1995; 95US-00472802.

PR 07-JUN-1995; 95US-00482115.

XX (GERO-) GERON CORP.

XX VILLEPONTIEU B, FENG J, FUNK W, ANDREWS WH;

XX WPI; 1996-097581/10.

PT RNA component of mammalian telomerase, esp. human - useful in identifying

XX e.g. candidate telomerase-modulating agents.

XX Claim 14; Page 97-98; 114pp; English.

XX The present sequence is the gene for the RNA component of human

XX telomerase (RCHT), which was derived from a genomic DNA library obtd.

XX from the human lung fibroblast cell line WI-38. The gene and the RCHT can

XX be used in the recombinant prodn. of an active telomerase mol., capable

XX of adding sequences to chromosomal DNA telomeres, and in the synthesis of

XX mutant sequences for the detection of mutant mammalian telomerase RNA

XX component polynucleotides. The RCHT may also be used in the

XX identification of telomerase modulating agents, and in the detection of

XX telomerase related, or neoplastic conditions in a patient.

XX Polynucleotides of at least 25 consecutive nucleotides identical, or

XX complementary to the RCHT sequence linked to heterologous transcriptional

XX regulatory sequences, can be used for the gene therapy of human diseases

XX Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 U; 0 Other;

XX Query Match 96.3%; Score 834.6; DB 2; Length 2425;

XX Best Local Similarity 99.0%; Pred. No. 6.7e-257;

XX Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

QY 1 AACTCTGAGAGGCTGAGACGAGATCGCTTGAACCCGGGAGGACAGGTTGCAGTG 60

Db 662 AACTACTGAGAGGCTGAGACGAGATCGCTTGAACCCGGGAGGACAGGTTGCAGTG 720

QY 61 AGCCGAGATCAGCCACTGACTCCATCCAGCTGGGCGAAGAGACAGACTCCGCTCA 120

Db 721 AGCCGAGATCAGCCACTGACTCCATCCAGCTGGGCGAAGAGACAGACTCCGCTCA 780

QY 121 AAAAAAAAAATCGTTACAAATTATAGTGATTAATCTCCCTCTTTTACTCTCAAGACA 180

Db 781 AAAAAAAAAATCGTTACAAATTATAGTGATTAATCTCCCTCTTTTACTCTCAAGACA 840

QY 181 CAGCACTACTTTAAAGCAAGTCATGATTTGAAGGCTTTCTTTCTTAATAAAGGAG 240

Db 841 CAGCACTACTTTAAAGCAAGTCATGATTTGAAGGCTTTCTTTCTTAATAAAGGAG 900

QY 241 ATTCACTCTTAAGATTAATTAATAGTAGTACCTGATTAAGCCATCTGCTCA 300

Db 901 ATTCACTCTTAAGATTAATTAATAGTAGTACCTGATTAAGCCATCTGCTCA 960

QY 301 AGGAGAGCTGAGAAAGGCAATTTAGAGAAAAAGGCGAGGGTTGAACTGGAGCATC 360

Db 961 AGGAGAGCTGAGAAAGGCAATTTAGAGAAAAAGGCGAGGGTTGAACTGGAGCATC 1020

QY 361 CCACTGAGCCGAGACAAAGATTCTGCTAGTACGAGTGGCTGGGAATCTATTTTCACA 420

Db 1021 CCACTGAGCCGAGACAAAGATTCTGCTAGTACGAGTGGCTGGGAATCTATTTTCACA 1080

QY 421 AGTTCTCAAAAAATGTGATGATCAAACTAGAAATTAGTGTCTGTCTTAGGCCCTTA 480

Db 1081 AGTTCTCAAAAAATGTGATGATCAAACTAGAAATTAGTGTCTGTCTTAGGCCCTTA 1140

QY 481 AATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGTCGACA 540

Db 1141 AATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGCTGTGTCGACA 1200

QY 541 GGATGAAAAAAGGCGCTCTGATACCTCAAGTATGTTACCTTTAAAGAGTGGAG 600

Db 1201 GGATGAAAAAAGGCGCTCTGATACCTCAAGTATGTTACCTTTAAAGAGTGGAG 1260

QY 601 TAAAGACGAAAGCTTTTCCGAGCTGCGAGGCGAAGGCAAGCTCTTCTCATGCGGAA 660

Db 1261 TAAAGACGAAAGCTTTTCCGAGCTGCGAGGCGAAGGCAAGCTCTTCTCATGCGGAA 1320

QY 661 ATGAACTTTAATTCGCGGTTCCCGCCCAAGCGCCGCGAGAGGACTCTCAGAG 720

Db 1321 ATGAACTTTAATTCGCGGTTCCCGCCCAAGCGCCGCGAGAGGACTCTCAGAG 1380

QY 721 AGCCGAGAGTCAAGCTTGGCCAAATCCGTGCGGTGCGGCGCTCCCTTTAATAGCCGA 780

Db 1381 AGCCGAGAGTCAAGCTTGGCCAAATCCGTGCGGTGCGGCGCTCCCTTTAATAGCCGA 1440

QY 781 CTCGCCGCGGACCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 836

Db 1441 CTCGCCGCGGACCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 1500

QY 837 TTTTGTCTAACCTTAACCTGAGAAAGGCGTA 867

Db 1501 TTTTGTCTAACCTTAACCTGAGAAAGGCGTA 1531

RESULT 7

AAV41194
 ID AAV41194 standard; DNA; 961 BP.

AC AAV41194;

XX 08-OCT-1998 (first entry)

XX Pecti Fragment containing RNA component of human telomerase (hTR).

XX RNA component; human telomerase; antisense oligonucleotide; infection;

XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;

XX contrageption; sterilisation; immunosuppression; therapeutic; hTR;

XX immune system down-regulation; anti-inflammatory therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX misc_feature 266..716


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Db      121  GCCGGAATGGAATTATTTCCCTTCCCGCCCAACACCGCCGCCGAGAGAGTCACTC 180
Qy      714  TCACGAGAGCCCGGAGAGTCACTTGGCCCATCCGTCGCGTCCGCGCGCTCCCTTAT 773
Db      181  TCACGAGAGCCCGGAGAGTCACTTGGCCCATCCGTCGCGTCCGCGCGCTCCCTTAT 240
Qy      774  AAGCCGACTGCGCCGAGCGCACCGGGTTGCGGAGGGGTGGGCTGGGAGGGGTGGG 833
Db      241  AAGCCGACTGCGCCGAGCGCACCGGGTTGCGGAGGGGTGGGCTGGGAGGGGTGGG 300
Qy      834  CATTTTGTCTTAACCTTAAGAGAGGCGGTA 867
Db      301  CATTTTGTCTTAACCTTAAGAGAGGCGGTA 334

RESULT 9
AAS09471 ID AAS09471 standard; DNA; 980 BP.
AC AAS09471;
XX
XX
XX 24-OCT-2001 (first entry)
DE Human DNA containing the RNA component of telomerase.
XX
XX Human; Telomerase; RNA component; vaccine; antibody; cancer; EF2H;
XX nucleolin; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 21 /tag= a
FT misc_feature /note= "Designated 0 in the specification, with 7 in the
FT complementary strand"
FT 311..320 /tag= b
FT /label= Template region
FT /note= "This region is not further defined in the
FT specification"
XX
XX US6261556-B1.
XX
XX 17-JUL-2001.
XX
XX 18-OCT-1999; 99US-00420056.
XX
XX 04-AUG-1995; 95US-00510736.
XX
XX 04-APR-1997; 97US-00833377.
XX
XX (GERO-) GERON CORP.
XX
XX Weirich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA,
XX Kealey JT;
XX
XX WPI; 2001-450477/48.
XX
XX Purified human telomerase, useful for inducing immune response in
XX animals, comprises several thousand folds increased purity compared with
XX cytoplasmic crude cell preparations.
XX
XX Disclosure; Col 9-12; 29pp; English.
XX
XX The sequence contains human telomerase, hTR, RNA component. The invention
XX relates to a purified human telomerase core enzyme protein comprising
XX 2000-fold increased purity compared with a crude extract of cells from
XX adenovirus-transformed kidney cell line (293 cells) and when associated
XX with telomerase RNA component has DNA polymerase activity and a molecular
XX weight of 200-2000 Kilo Daltons (Kda). The purified telomerase is useful
XX for inducing a humoral or cell-mediated immune response in an animal.
XX Purified telomerase or immunogenic fragments are useful as vaccines for
XX treating diseases associated with over-expression of telomerase, such as
XX cancer and for producing antibodies that recognize telomerase, which are

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CC useful as affinity agents in isolating the proteins and for detecting the
CC presence of proteins in a sample, such as cell or tissue. Identification
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC Telomerase and/or telomerase associated proteins are also useful for
CC screening compounds to identify agents that alter the association of
CC telomerase-associated proteins, such as nucleolin or EF2H with telomerase
XX
XX Sequence 980 BP; 171 A; 303 C; 305 G; 200 T; 0 U; 1 Other;
XX
XX Query Match 38.4%; Score 333; DB 4; Length 980;
XX Best Local Similarity 99.7%; Pred. No. 7e-96;
XX Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy      534  CTCGAGAGATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTCACTTAAAGAG 593
Db      1  CTCGAGAGATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTCACTTAAAGAG 60
Qy      594  TCGGAAGTAAAGCAAGCAAGCCTTCCCGAGCGTCCGGAAGGGCAAGCTCTCTCARG 653
Db      61  TCGGAAGTAAAGCAAGCAAGCCTTCCCGAGCGTCCGGAAGGGCAAGCTCTCTCARG 120
Qy      654  GCCGGAATGGAATTATTTCCGTTCCCGCCCAACGACCGCCCGAGAGAGTCACTC 713
Db      121  GCCGGAATGGAATTATTTCCGTTCCCGCCCAACGACCGCCCGAGAGAGTCACTC 180
Qy      714  TCACGAGAGCCCGGAGAGTCACTTGGCCCATCCGTCGCGTCCGCGCGCTCCCTTAT 773
Db      181  TCACGAGAGCCCGGAGAGTCACTTGGCCCATCCGTCGCGTCCGCGCGCTCCCTTAT 240
Qy      774  AAGCCGACTGCGCCGAGCGCACCGGGTTGCGGAGGGGTGGGCTGGGAGGGGTGGG 833
Db      241  AAGCCGACTGCGCCGAGCGCACCGGGTTGCGGAGGGGTGGGCTGGGAGGGGTGGG 300
Qy      834  CATTTTGTCTTAACCTTAAGAGAGGCGGTA 867
Db      301  CATTTTGTCTTAACCTTAAGAGAGGCGGTA 334

RESULT 10
AAD24234 ID AAD24234 standard; DNA; 981 BP.
AC AAD24234;
XX
XX
XX 07-MAR-2002 (first entry)
DE Human telomerase (hTR) gene.
XX
XX Human; telomerase; TR; telomerase activity-related disease; therapy;
XX cancer; pregnancy; fertility; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 267..715 /tag= a
FT misc_feature /note= "hTR transcript serves as template in the
FT telomerase ribonucleoprotein"
XX
XX US6300110-B1.
XX
XX 09-OCT-2001.
XX
XX 23-DEC-1998; 98US-00220157.
XX
XX 09-SEP-1995; 95US-0003492P.
XX
XX 05-JAN-1996; 96US-00583808.
XX
XX 13-SEP-1996; 96US-00710249.
XX
XX (GERO-) GERON CORP.
XX
XX Villeponteau B, Feng J, Andrews WH, Adams RR;
XX

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WPI; 2002-033174/04.

Reptide products of the human TPC2 and TPC3 gene are involved in regulation of telomere length and activity are useful to diagnose and treat telomere length and activity-related diseases.

Example; Fig 9; 60pp; English.

The invention relates to methods and reagents for regulating telomere length and for modulating telomerase activity in mammalian cells. The invention also relates to purified, synthetic or recombinant peptides such as TPC2 or TPC3 used for detecting regulators of telomere length and telomerase activity in mammalian cells and for a variety of related diagnostic and therapeutic purposes. The method is useful for screening, diagnosing, monitoring and treating diseases and other conditions such as cancer, pregnancy, fertility, telomere length and telomerase-activity. The present sequence is human telomerase (hTR) gene

Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

Query Match

Best Local Similarity 38.4%; Score 333; DB 6; Length 981;

Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 534 CTGCAGAGATGAAAAAGGCCCTGTATACCTCAAGTTAGTTTCACTTTAAAGAG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTGTATACCTCAAGTTAGTTTCACTTTAAAGAG 60
QY 594 TCGGAAGTAAAGACGCAAGCCCTTCCCGACGTGGGAAAGGCAAGTCTTCTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCCTTCCCGACGTGGGAAAGGCAAGTCTTCTCATG 120
QY 654 GCCGGAATGAAAGCTTTAATTTCCGTTCCCGCAACAGCCCGCGGAGAGTACTC 713
DB 121 GCCGGAATGAAAGCTTTAATTTCCGTTCCCGCAACAGCCCGCGGAGAGTACTC 180
QY 714 TCACGAGAGCCCGGAGAGTCACTTGGCCCAATCCGTGGGTGGCGGCGCTCTTAT 773
DB 181 TCACGAGAGCCCGGAGAGTCACTTGGCCCAATCCGTGGGTGGCGGCGCTCTTAT 240
QY 774 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTGGAGGGTGTGGC 833
DB 241 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTGGAGGGTGTGGC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 334

```

RESULT 11

AA89242
ID AAT89242 standard; DNA; 981 BP.

AC AAT89242;

XX 12-MAY-1998 (first entry)

DE Clone containing hTR sequence.

KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridization;
inhibitor; human telomerase RNA; hTR; ds.

OS Synthetic.

OS Homo sapiens.

DE Key Location/Qualifiers

FT misc_difference 255..716

FT /tag= a

FT /note= "human telomerase RNA"

PN WO9738013-A1.

XX 16-OCT-1997.

XX 09-APR-1997; 97WO-US005931.

XX 09-APR-1996; 96US-00630019.

XX (GERO-) GERON CORP.

PI Shay JW, Wright WE, Piatyzek MA, Corey D, Norton JC;

DR WPI; 1997-512647/47.

XX New peptide nucleic acid hybridising to mammalian telomerase RNA - used

PT to inhibit telomerase, for treating tumours and other proliferative

PS diseases, also for diagnosis.

XX disclosure; Page 20-21; 76pp; English.

This fragment of cloned DNA contains the human telomerase RNA (hTR) sequence, (266-716bp). The hTR region contains a CCC template which the peptide nucleic acid (PNA) can recognise. The presence of a GGG in the PNA allows for the specific hybridisation to the template region of this hTR component. PNAs can be used as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, especially in the treatment of cancer

Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

Query Match

Best Local Similarity 38.3%; Score 332.4; DB 2; Length 981;

Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 534 CTGCAGAGATGAAAAAGGCCCTGTATACCTCAAGTTAGTTTCACTTTAAAGAG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTGTATACCTCAAGTTAGTTTCACTTTAAAGAG 60
QY 594 TCGGAAGTAAAGACGCAAGCCCTTCCCGACGTGGGAAAGGCAAGTCTTCTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCCTTCCCGACGTGGGAAAGGCAAGTCTTCTCATG 120
QY 654 GCCGGAATGAAAGCTTTAATTTCCGTTCCCGCAACAGCCCGCGGAGAGTACTC 713
DB 121 GCCGGAATGAAAGCTTTAATTTCCGTTCCCGCAACAGCCCGCGGAGAGTACTC 180
QY 714 TCACGAGAGCCCGGAGAGTCACTTGGCCCAATCCGTGGGTGGCGGCGCTCTTAT 773
DB 181 TCACGAGAGCCCGGAGAGTCACTTGGCCCAATCCGTGGGTGGCGGCGCTCTTAT 240
QY 774 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTGGAGGGTGTGGC 833
DB 241 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTGGAGGGTGTGGC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 334

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RESULT 12

AAV63644
ID AAV63644 standard; DNA; 981 BP.

AC AAV63644;

XX 15-FEB-1999 (first entry)

DE Human telomerase RNA component sequence from lambda clone 28-1.

KW Lambda clone 28-1; human; telomerase RNA component; anticancer therapy;

OS assay; vaccine; cancer; purification; ss.

OS Synthetic.

OS Homo sapiens.

DE Key Location/Qualifiers

```
FT misc_feature 266..716
FT FT /**tag=
XX /note="human telomerase RNA component sequence"
XX PN WO9845450-A1.
XX PD 15-OCT-1998.
XX PF 04-APR-1997; 97WO-US006012.
XX PR 04-APR-1997; 97WO-US006012.
XX PA (GERO-) GERON CORP.
XX PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA,
XX PI Kealey JT;
XX DR WPI; 1998-594485/50.
XX PT Purification of telomerase on affinity material - useful for, e.g.
XX PT diagnosis and treatment of cancer.
XX PS Disclosure; Page 14-15; 76pp; English.
XX CC The present sequence represents the PstI fragment of the 2.4 Kb SauIIAI-
XX CC HindIII fragment of lambda clone 28-1. This clone contains human
XX CC telomerase RNA component gene sequences. The specification provides
XX CC methods for purifying human telomerase. The methods involve the use of
XX CC several sequential steps, including the use of two matrices that bind
XX CC molecules bearing negative charges, a matrix that binds molecules bearing
XX CC positive charges, an affinity purification step and a size separation.
XX CC Telomerase is a particular target of anticancer therapies, and is useful
XX CC in assays for characterizing (pre)cancerous cells. The present sequence
XX CC can be used for such assays. Telomerase can also be used to screen for
XX CC specific modulators, for biochemical analysis of its activity, and in
XX CC preparation of antibodies. Fragments of telomerase, or nucleic acid
XX CC encoding them, are used in vaccines, and for treating over expression of
XX CC telomerase, particularly in cancer
XX SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

Query Match 38.3%; Score 332.4; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.1e-95;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 593
DB 1 CTGCAGAGATGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 60
QY 594 TCGAAGTAAAGACGCAAGCCCTTCCCGACGTGCGAAGGCAAGTCCTTCATG 653
DB 61 TCGAAGTAAAGACGCAAGCCCTTCCCGACGTGCGAAGGCAAGTCCTTCATG 120
QY 654 GCCGGAATGGAACCTTAATTTCCGTTCCCGCAACAGCCCGCGAGAGATGATC 713
DB 121 GCCGGAATGGAACCTTAATTTCCGTTCCCGCAACAGCCCGCGAGAGATGATC 180
QY 714 TCACGAGACCGCGAGAGTCAAGTTCGCAATCCGTCGCGCGCGCTCCCTTAT 773
DB 181 TCACGAGACCGCGAGAGTCAAGTTCGCAATCCGTCGCGCGCGCTCCCTTAT 240
QY 774 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTTGGAGGGGTGGGC 833
DB 241 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTTGGAGGGGTGGGC 300
QY 834 CATTTTGTCTAACCTTAACCTGAGAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAACCTGAGAGGGCGTA 334

RESULT 13
AAZ23626
ID AAZ23626 standard; DNA; 981 BP.
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XX AC AAZ23626;
XX XX 07-JAN-2000 (first entry)
XX DT Human clone 28-1 containing telomerase fragment.
XX DE Telomerase; human; immune response; cancer; vaccine; treatment; disease;
XX KW ss.
XX OS Homo sapiens.
XX PN US968506-A.
XX PD 19-OCT-1999.
XX PF 04-APR-1997; 97US-00833377.
XX PR 04-AUG-1995; 95US-00510736.
XX PA (GERO-) GERON CORP.
XX PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT,
XX PI Vassero AP;
XX DR WPI; 1999-590379/50.
XX PT Compositions comprising human telomerase, useful for treating diseases
XX PT associated with overexpression of telomerase e.g. cancer.
XX PS Disclosure; Col 41-42; 34pp; English.
XX CC This invention describes a novel composition comprising human telomerase
XX CC having at least 2000-fold (preferably at least 6000-fold) increased
XX CC relative purity compared with crude extract of cells from adenovirus-
XX CC transformed kidney cell line. The composition is useful for eliciting an
XX CC immune response in animals and may therefore be used as a vaccine for
XX CC treating diseases associated with the overexpression of telomerase e.g.
XX CC cancer. This sequence represents a nucleic acid fragment from human clone
XX CC 28-1 which contains a fragment of the human telomerase described in the
XX CC method of the invention
XX SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

Query Match 38.3%; Score 332.4; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.1e-95;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 593
DB 1 CTGCAGAGATGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 60
QY 594 TCGAAGTAAAGACGCAAGCCCTTCCCGACGTGCGAAGGCAAGTCCTTCATG 653
DB 61 TCGAAGTAAAGACGCAAGCCCTTCCCGACGTGCGAAGGCAAGTCCTTCATG 120
QY 654 GCCGGAATGGAACCTTAATTTCCGTTCCCGCAACAGCCCGCGAGAGATGATC 713
DB 121 GCCGGAATGGAACCTTAATTTCCGTTCCCGCAACAGCCCGCGAGAGATGATC 180
QY 714 TCACGAGACCGCGAGAGTCAAGTTCGCAATCCGTCGCGCGCGCTCCCTTAT 773
DB 181 TCACGAGACCGCGAGAGTCAAGTTCGCAATCCGTCGCGCGCGCTCCCTTAT 240
QY 774 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTTGGAGGGGTGGGC 833
DB 241 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGAGGTGGCTTGGAGGGGTGGGC 300
QY 834 CATTTTGTCTAACCTTAACCTGAGAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAACCTGAGAGGGCGTA 334
```

RESULT 14
 ID AAA37564
 AC AAA37564 standard; DNA; 981 BP.
 AC AAA37564;
 DT 15-AUG-2000 (first entry)
 XX Human telomerase nucleotide sequence.
 DE
 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ds.
 OS Homo sapiens.
 XX
 PN US6046307-A.
 XX
 PD 04-APR-2000.
 XX
 PF 09-APR-1997; 97US-00838545.
 XX
 PR 09-APR-1996; 96US-00630019.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Wright WE, Platyszek MA, Shay JW, Norton JC, Corey DR;
 FI WPI; 2000-292432/25.
 DR
 PT New peptide nucleic acid (PNA) compounds that inhibit telomerase activity
 PT in mammalian cells is useful as probes to detect the RNA component of a
 PT mammalian telomerase.
 PS
 PS Disclosure; Col 13-14; 45pp; English.
 XX
 CC The present sequence represents the human telomerase nucleotide sequence.
 CC The invention relates to peptide nucleic acid molecules which hybridize
 CC to the mRNA component of mammalian telomerase, and inhibit telomerase
 CC activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one
 CC strand of the telomeric DNA, using as a template an 11 nucleotide
 CC sequence contained within the RNA component of the enzyme. The invention
 CC relates to PNA molecules having a sequence of no more than 25 bases,
 CC which include the sequence GTTAGG. The uncharged nature of the PNA
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancer, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
 CC syndrome) and associated pathological, fungal infections, and other
 CC diseases characterized by abnormal telomere metabolism or telomerase
 CC activity, in combination with antineoplastic and other cytotoxic or
 CC cytostatic agents, antifungal agents, and other nucleosides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (htr) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on htr gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component
 XX
 SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;
 Query Match 38.3%; Score 332.4; DB 3; Length 981;
 Best Local Similarity 99.7%; Pred. No. 1.1e-95;

Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 61 TCGAAGTAAAGACGCAAGGCTTTCCGGAAGTGGGAAGGCAAGTCTCTCATG 120
 QY 654 GCGGAATGAACTTTAAATTTCCGTTCCCGCAACGAGCCCGCGAGAGTGAATC 713
 DB 121 GCGGAATGAACTTTAAATTTCCGTTCCCGCAACGAGCCCGCGAGAGTGAATC 180
 QY 714 TCACGAGAGCCGGAAGTCAAGTTGGCCAAATCCGTCGGCGGCGCTCTCTTAT 773
 DB 181 TCACGAGAGCCGGAAGTCAAGTTGGCCAAATCCGTCGGCGGCGCTCTCTTAT 240
 QY 774 AAGCGACTCGCCCGGACGCGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG 833
 DB 241 AAGCGACTCGCCCGGACGCGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 QY 834 CATTTTGTCTTAACCTTAAGTGAAGGCGCTA 867
 DB 301 CATTTTGTCTTAACCTTAAGTGAAGGCGCTA 334
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 AC AAS15442 standard; DNA; 981 BP.
 AC AAS15442;
 DT 14-FEB-2002 (first entry)
 XX
 DE Pecti fragment containing human telomerase RNA component gene sequence.
 XX
 KW Mammalian; forensic; paternity testing; human telomerase RNA component;
 KW htr gene RFLP pattern; cancer; inflammation; lymphoproliferative disease;
 KW autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia;
 KW HIV; AIDS; human immunodeficiency virus; telomere metabolism; cytostatic;
 KW acquired immunodeficiency syndrome; anti-inflammatory; immunosuppressive;
 KW bacteriophage lambda clone 28-1; ds.
 OS Homo sapiens.
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 FT /note= "htr gene sequence"
 FT /*tag= b
 FT /note= "Template region of htr used as template for
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 PN US6294650-B1.
 XX
 PD 25-SEP-2001.
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 PF 08-JUL-1999; 99US-00349532.
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 PR 09-APR-1996; 96US-00630019.
 PR 09-APR-1997; 97US-00838545.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC;
 FI WPI; 2001-638024/73.
 DR
 PT New peptide nucleic acids that hybridizes to the RNA component of
 PT mammalian telomerase, useful for treating or preventing cancer,
 PT inflammation, lymphoproliferative diseases, autoimmune disease, or

PT neurodegenerative diseases.

XX Disclosure; Col 13-16; 46pp; English.

CC The present invention relates to peptide nucleic acids (PNAs), comprising
CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC mammalian cells by hybridising to the RNA component of mammalian
CC telomerase. The PNAs are useful as probes to detect the RNA component of
CC mammalian telomerase and as inhibitors of telomerase activity, or to
CC detect and/or quantitate polynucleotide having the human telomerase RNA
CC component (hTR) sequence, as well as in forensic identification of
CC individuals, such as paternity testing or identification of criminal
CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC PNA can be further used for treating or preventing cancer, inflammation,
CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC diseases. The PNAs in combination with other pharmaceuticals (such as
CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents a Peti fragment, derived from
CC bacteriophage lambda clone 28-1, containing the hTR gene sequence
XX

SQ Sequence 981 BP; 172 A; 303 G; 305 G; 200 T; 0 U; 1 Other;

Query Match 38.3%; Score 332.4; DB 4; Length 981;

Best Local Similarity 99.7%; Pred. No. 1,1e-95;

Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAGAAGG 593
DB 1 CTGCAAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAGAAGG 60
QY 594 TCGAAGTAAAGCGCAAGCCCTTCCCGGACGTGCGAAGGCAAGTCTTCTCATG 653
DB 61 TCGAAGTAAAGCGCAAGCCCTTCCCGGACGTGCGAAGGCAAGTCTTCTCATG 120
QY 654 GCCGAAATGAACTTTAATTTCCCGTCCCGCAACAGCCCGCGGAGAGTATC 713
DB 121 GCCGAAATGAACTTTAATTTCCCGTCCCGCAACAGCCCGCGGAGAGTATC 180
QY 714 TCACGAGAGCCGCGAAGTCACTTGCCCATCCGTGCGGTGCGCGCTCCCTTAT 773
DB 181 TCACGAGAGCCGCGAAGTCACTTGCCCATCCGTGCGGTGCGCGCTCCCTTAT 240
QY 774 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGGTTGGGCTGGAAGGGTGTGGC 833
DB 241 AAGCCGACTCGCCCGGACGCAACCGGTTGCGAGGTTGGGCTGGAAGGGTGTGGC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGGCGTA 334

Search completed: April 26, 2005, 16:28:00
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Run on: April 26, 2005, 16:01:02 ; Search time 4148.84 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	867	6	BD225833 Promoter
2	867	100.0	867	6	AX019582 Sequence
3	867	100.0	1765	6	BD225798 Promoter
4	867	100.0	1765	6	AX019547 Sequence
5	867	100.0	1765	6	AF047386 Homo sapi
6	860.6	99.3	47601	9	AC078802 Homo sapi
7	848.6	97.9	2420	6	I31750 Sequence 3
8	848.6	97.9	2426	6	AR016035 Sequence
9	848.6	97.9	2426	6	AR059196 Sequence
10	848.6	97.9	2426	6	AR075507 Sequence
11	848.6	97.9	2426	6	AR081664 Sequence
12	848.6	97.9	2426	6	AR161905 Sequence
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14	834.6	96.3	2425	6	BD176144 Mammalian
15	334	38.5	981	6	AR081665 Sequence
16	334	38.5	981	6	BD023697 Method fo
17	333	38.4	981	6	AR028774 Sequence
18	333	38.4	981	6	AR369711 Sequence
19	333	38.4	981	6	AX022166 Sequence

20	332.4	38.3	981	6	A84591 Sequence 1
21	332.4	38.3	981	6	AR063825 Sequence
22	332.4	38.3	981	6	AR079888 Sequence
23	332.4	38.3	981	6	BD058132 Purified
24	332.4	38.3	981	6	BD071055 Modulator
25	176	20.3	176	6	BD225836 Promoter
26	176	20.3	176	6	AX019585 Sequence
27	166	19.1	548	9	AF221907 Homo sapi
28	163	18.8	545	9	HSU86046 Human telom
29	120	13.8	120	6	BD225878 Promoter
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31	117.2	13.5	157466	2	AC004888 Homo sapi
32	115.6	13.3	54047	2	AC136293 Homo sapi
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34	115.6	13.3	70778	2	AC133136 Homo sapi
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37	115.6	13.3	188571	2	AC107956 Homo sapi
38	114.2	13.2	197099	9	AL136979 Human DNA
39	114	13.1	115812	9	AC004796 Homo sapi
40	113.6	13.1	176550	9	AL356356 Human DNA
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ALIGNMENTS

RESULT 1	BD225833	867 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD225833	Promoter	region of mouse and human telomerase RNA component genes.		
DEFINITION	BD225833	Promoter	region of mouse and human telomerase RNA component genes.		
ACCESSION	BD225833.1	GI:33035603			
VERSION	BD225833.1	GI:33035603			
KEYWORDS	JP 2002509699-A/36.				
SOURCE	JP 2002509699-A/36.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 867)				
JOURNAL	Promoter region of mouse and human telomerase RNA component genes				
COMMENT	Patent: JP 2002509699-A 36 02-APR-2002; CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD OS Homo sapiens (human) PN JP 2002509699-A/36 PD 02-APR-2002 PF 29-JAN-1999 JP 2000529424 PR 29-JAN-1998 GB 9801902.9 PI WILLIAM NICOL KEITH				
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Best Local Similarity	100.0%; Pred. No. 3.7e-238;				

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Db	421	AGTTCTCCAAAATGATGATCAAACTAGAAATTAATTA	ATTAATTTTCA	480					
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ORIGIN

REFERENCE
1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS
1 Keith, W.N.
TITLE
Promoter regions of the mouse and human telomerase rna component
JOURNAL
Genes
Patent: WO 938964-A 36 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES
1. 867
Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 100.0%; Score 867; DB 6; Length 867;
Best Local Similarity 100.0%; Pred. No. 3.7e-238;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS	BD225798	1765 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Promoter region of mouse and human telomerase RNA component genes.				
ACCESSION	BD225798				
VERSION	BD225798.1				
KEYWORDS	JP 2002509699-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (basee 1 to 1765)				
TITLE	Keith, W.N.				
JOURNAL	Promoter region of mouse and human telomerase RNA component genes Patent: JP 2002509699-A 1 02-APR-2002; CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD				
COMMENT	OS Homo sapiens (human) PN JP 2002509699-A/1 PD 02-APR-2002 PF 29-JAN-1999 JP 2000529424 PR 29-JAN-1998 GB 9801902.9 PI WILIAM NICOL KEITH PC C12N15/09, A61K31/7105, A61K31/711, A61K35/76, A61K38/00, A61K45/00, PC A61K48/00, PC A61P35/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02 PC C12O1/68//C12N9/12. PC (A61K35/76, A61K31.522), C12N15/00, A61K37/02, C12N5/00 CC Promoter region of mouse and human telomerase RNA component genes				
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Db	841	TGCTTAACCTTAATCTAGAGAGGCGGTA	867
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DEFINITION	Sequence 1 from Patent WO938964.		
ACCESSION	AX019547		
VERSION	AX019547.1	GI:10043461	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.		
JOURNAL	Keith, W.N.		
FEATURES	Promoter regions of the mouse and human telomerase rna component		
source	genes: WO 938964-A 1 05-AUG-1999;		
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 AF047386
 ACCESSION AF047386.1 GI:300555
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1765)
 AUTHORS Zhao J.O., Hoare S.F., McFarlane R., Muir S., Parkinson E.K.,
 Black D.M. and Keith W.N.
 TITLE Cloning and characterization of human and mouse telomerase RNA gene
 promoter sequences
 JOURNAL Oncogene 16 (10), 1345-1350 (1998)
 MEDLINE 98206512

PUBMED 9546436
 REFERENCE 2 (bases 1 to 1765)
 AUTHORS Zhao J.O., Hoare S.F., McFarlane R., Muir S., Parkinson E.K.,
 Black D.M. and Keith W.N.
 TITLE Direct Submission
 JOURNAL Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
 Switchback Rd, Glasgow G61 1BD, UK
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ORIGIN
 Query Match 100.0%; Score 867; DB 9; Length 1765;
 Best Local Similarity 100.0%; Pred. No. 4.3e-238; Mismatches 0; Gaps 0;
 Matches 867; Conservative 0; Indels 0;

QY 1 AGTACTCAGAGGCTGAGACAGCAAGATCGTTGAACCGGAGGAGGAGAGTGCAGTG 60
 Db 1 AGTACTCAGAGGCTGAGACAGCAAGATCGTTGAACCGGAGGAGGAGAGTGCAGTG 60
 QY 61 AGCGAGATCAGCGCATGACCTCATCAGCTGCGCGAAGAGCAAGCTCGTCTCA 120
 Db 61 AGCGAGATCAGCGCATGACCTCATCAGCTGCGCGAAGAGCAAGCTCGTCTCA 120
 QY 61 AGCGAGATCAGCGCATGACCTCATCAGCTGCGCGAAGAGCAAGCTCGTCTCA 120
 Db 61 AGCGAGATCAGCGCATGACCTCATCAGCTGCGCGAAGAGCAAGCTCGTCTCA 120
 QY 121 AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTCTTTTACTCATCAAGACA 180
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DEFINITION Homo sapiens 3 BAC RP11-81606 (Roswell Park Cancer Institute Human
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VERSION   AC078802.14 GI:28626602
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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 47601)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
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Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Dayala, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X.,
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Hollins, B., Homs, F., Howard, S., Huber, J., Hui, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovach, J.,
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Lewis, L., Li, J., Li, Z., Lichtharge, O., Lieu, C., Liu, J., Liu, W.,
Louiseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A.,
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Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E.,
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Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C.,
Taylor, T., Telford, B., Thomas, N., Thomas, S., Uman, K., Vasquez, L.,
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Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.,
Wu, Y.F., Zhou, J., Zorrilla, S., Zorrilla, S.L., Zorrilla, G. and
Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 47601)
Worley, K.C.

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TITLE
JOURNAL
Submitted (04-AUG-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 47601)
AUTHORS
Worley, K.C.
TITLE
Direct Submission
JOURNAL
Submitted (22-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 47601)
REFERENCE
Worley, K.C.
AUTHORS
Worley, K.C.
TITLE
Direct Submission
JOURNAL
Submitted (01-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 1, 2003 this sequence version replaced gi:28467099.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu

COMMENT
CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated quality individual bases and measures of base
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
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Unclassified.

REFERENCE 1 (bases 1 to 2420)

Vilpenteau B., Feng, J., Funk, W. and Andrews, W. H.

Mammalian telomerase

JOURNAL Patent: US 5583016-A 3 10-DEC-1996;

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ORIGIN

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

Vilpenteau B., Feng, J., Funk, W. and Andrews, W. H.

Asays for the DNA component of human telomerase

JOURNAL Patent: US 5776679-A 3 07-JUL-1998;

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Best Local Similarity 99.4%; Pred. No. 8.9e-233;

Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTGAGAGGCTGAGACACGAGATCGCTTGAACCCGGGAGGAGAGGTTGCACTG 60
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 QY 601 TAAAGACGCAAGCTTTTCCCGAGAGTGGGAGAGGCAACGTCCTTCTCATAGGCCGAA 660
 DB 1261 TAAAGACGCAAGCTTTTCCCGAGAGTGGGAGAGGCAACGTCCTTCTCATAGGCCGAA 1320
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[illegible]

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Db	1201	GGATTGAAAAAAGGCCCTCTGTATCTCAAGTTAGTTTCACTTTTAAAGAAAGTCGGAAG	1260
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QY	661	ATGGAACCTTAAATTTCCGCTTCCGCAACCAACGACCCCGGAGAGAGTGACTTCAACGAG	720
Db	1321	ATGGAACCTTAAATTTCCGCTTCCGCAACCAACGACCCCGGAGAGAGTGACTTCAACGAG	1380
QY	721	AGCGCGAGAGTCACTCTGGCCAAATCCGTCGTGCGGCGCGCTCCCTTTATTAAGCCGA	780
Db	1381	AGCGCGAGAGTCACTCTGGCCAAATCCGTCGTGCGGCGCGCTCCCTTTATTAAGCCGA	1440
QY	781	CTGCGCCGCGACGCGACCGGTTGCGAGGGTGGGCTCGGAGGGGGTGGTGGCATTTT	840
Db	1441	CTGCGCCGCGACGCGACCGGTTGCGAGGGTGGGCTCGGAGGGGGTGGTGGCATTTT	1500
QY	841	TGCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA	900
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RESULT 10			
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LOCUS	AR075507	2426 bp	DNA linear PAT 30-AUG-2000
DEFINITION	Sequence 4 from patent US 5958680.		
ACCESSION	AR075507		
VERSION	AR075507.1	GI:10002257	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2426)		
AUTHORS	Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.		
TITLE	Mammalian telomerase		
JOURNAL	Patent: US 5958680-A 4 28-SEP-1999;		
FEATURES	Location/Qualifiers		
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Best Local Similarity	99.4%; Pred. No. 8,9e-233;		
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QY	61	AGCGGAGATCACGCGCATAGACTTCATCCAGCCCTGGCGGGAAGCAAGCTCGCTCTCA	120
Db	721	AGCGGAGATCACGCGCATAGACTTCATCCAGCCCTGGCGGGAAGCAAGCTCGCTCTCA	780
QY	121	AAAAAATAATTCGTTACATTTATGTTGATTAATCCCTCTTTTAACTCATCAAGACA	180
Db	781	AAAAAATAATTCGTTACATTTATGTTGATTAATCCCTCTTTTAACTCATCAAGACA	840
QY	181	CAGACATCTTAAAGCAAGTCAATGATTTGAAGCGCTTTCTTCTTAATAAAGGAG	240
Db	841	CAGACATCTTAAAGCAAGTCAATGATTTGAAGCGCTTTCTTCTTAATAAAGGAG	900
QY	241	ATTCAAGCTTAAAGATTAATATGATGATGATCACTTGAATTAAGCAATCTCTGCTCA	300
Db	901	ATTCAAGCTTAAAGATTAATATGATGATGATCACTTGAATTAAGCAATCTCTGCTCA	960
QY	301	AGGAGAACTGAGAAAGCAATTTTAAAGAAAAAGGCGCAGGTTGAACTCGGACGCATC	360

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Db 1381 AGCCGCGAGATCAGCTTGGCCATCCGTCGCGGTGGGCGCGCTCTTTAATAAGCCGA 1440
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Qy 841 TGTCTAACCTTAAGTGAAGAGGCGCTA 867
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LOCUS AR081664
DEFINITION Sequence 1 from patent US 5972605.
ACCESSION AR081664
VERSION AR081664.1 GI:10008390
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeneuve,B. and Harley,C.
TITLE Assaye for regulators of mammalian telomerase expression
JOURNAL Patent: US 5972605-A 1 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..2426
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Best Local Similarity 99.4%; Pred. No. 8.9e-233;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 901 ATTCAGTCTTAAGATTAATATATGATGATTAACACTGATTAAGCAATCTCTGTCTCA 960
Qy 301 AGAAGAACCTGAGAGAGCATTTCTAAGAAAAAGGGGAGAGGGTGGAACTCGAGCGATC 360
Db 961 AGAAGAACCTGAGAGAGCATTTCTAAGAAAGGGGAGAGGGTGGAACTCGAGCGATC 1020
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Db 1021 CCAGTACGCGGAGCAAGATTCTGCTAGTACAGTGTGCGCTGGGAATCTATTTTACAA 1080
Qy 421 AGTTCTCCAAAAAATGTATGATCAAAACTAGAAATTTAGTGTCTGTGCTTAGGCCCTTA 480
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Qy 661 ATGAACTTTAATTTCCGCTTCCCGCAACGCGCGCGAGAGAGTACTCTCAGAG 720
Db 1321 ATGAACTTTAATTTCCGCTTCCCGCAACGCGCGCGAGAGAGTACTCTCAGAG 1380
Qy 721 AGCCGCGAGATCAGCTTGGCCATCCGTCGCGGTGGGCGCGCTCTTTAATAAGCCGA 780
Db 1381 AGCCGCGAGATCAGCTTGGCCATCCGTCGCGGTGGGCGCGCTCTTTAATAAGCCGA 1440
Qy 781 CTCGCCGCGAGCGCACCGGGTTGGAGAGGGTGGCTGAGAGGGGTGGTGGCCATTTT 840
Db 1441 CTCGCCGCGAGCGCACCGGGTTGGAGAGGGTGGCTGAGAGGGGTGGTGGCCATTTT 1500
Qy 841 TGTCTAACCTTAAGTGAAGAGGCGCTA 867
Db 1501 TGTCTAACCTTAAGTGAAGAGGCGCTA 1527

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LOCUS AR161905
DEFINITION Sequence 3 from patent US 6258535.
ACCESSION AR161905
VERSION AR161905.1 GI:16228915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeneuve,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 3 10-JUL-2001;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 97.9%; Score 848.6; DB 6; Length 2426;
Best Local Similarity 99.4%; Pred. No. 8.9e-233;

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REFERENCE
1 (bases 1 to 2426)
Vilpeotteau, B., Feng, J., Funk, W. and Andrews, W. H.
AUTHORS
Mammalian telomerase
TITLE
Patent: US 6548298-A 3 15-APR-2003;
JOURNAL
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FEATURES
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Db	662	AGCTACTCGAGGAGGCTGAGACACGAGAAATCGCTTGAAACCCGGGAGCGACAGATTGCACTG	720		
QY	61	AGCCGAGATCAGCCCATAGATCCATCATAGCTGGGGGAAAGAGCAAGATCCGCTTCA	120		
Db	721	AGCCGAGATCAGCCCATAGATCCATCATAGCTGGGGGAAAGAGCAAGATCCGCTTCA	780		
QY	121	AAAAAAAAAATCGTTACAATTTATGATGATTAATCTCCCTCTTTTAACTCATCAAGACA	180		
Db	781	AAAAAAAAAATCGTTACAATTTATGATGATTAATCTCCCTCTTTTAACTCATCAAGACA	840		
QY	181	CAGCACTACTTTAAAGCAAAAGTCATGATTTGAAACGCTTTCTTTCTAATAAAGGAG	240		
Db	841	CAGCACTACTTTAAAGCAAAAGTCATGATTTGAAACGCTTTCTTTCTAATAAAGGAG	900		
QY	241	ATTCACTCTTAAGTTAATATATGATGATTAAGTAACTTTAAGCATCTCTGCTCA	300		
Db	901	ATTCACTCTTAAGTTAATATGATGATTAAGTAACTTTAAGCATCTCTGCTCA	960		
QY	301	AGGAGAGCTGAGAGAGCATTTCTAAGGAAAAGGGGACGGGTGGAATCTCGAGCATC	360		
Db	961	AGGAGAGCTGAGAGAGCATTTCTAAGGAAAAGGGGACGGGTGGAATCTCGAGCATC	1020		
QY	361	CCACTGAGCCGAGACAAGATCTGCTGTAGTCAGTGCCTCGGGAACTATTATTCAAA	420		
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QY	481	AAATCTTCCTGTGAATTCATTTTAAAGTAAAGTGAACCGGCTCGTCTGCTGAGA	540		
Db	1141	AAATCTTCCTGTGAATTCATTTTAAAGTAAAGTGAACCGGCTCGTCTGCTGAGA	1200		
QY	541	GGATGAAAAAAGGCCCTCTGATACCTCAAGTTAAGTTCACTTTAAAGAAAGTCCGAA	600		
Db	1201	GGATGAAAAAAGGCCCTCTGATACCTCAAGTTAAGTTCACTTTAAAGAAAGTCCGAA	1260		
QY	601	TAAAGAGCAAAAGCCTTCCCGAGCGGAGGAGGCAAGTCTTCTCATATGACCGGAA	660		
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QY	661	ATGGAACTTTAATTTCCGTTCCGCCCAACACAGCCCGCCGAGAGAGTGACTTCAAG	720		
Db	1321	ATGGAACTTTAATTTCCGTTCCGCCCAACACAGCCCGCCGAGAGAGTGACTTCAAG	1380		
QY	721	AGCGGAGAGTCAAGCTTGGCCCAATCCGTGCGGCTCGGCGCGCTCCCTTTAATAGCGA	780		
Db	1381	AGCGGAGAGTCAAGCTTGGCCCAATCCGTGCGGCTCGGCGCGCTCCCTTTAATAGCGA	1440		
QY	781	CTGCGCCGAGAGCAACCGGTTGCGAGAGGATGAGGCTGAGAGGAGTGTGTCATTTT	840		
Db	1441	CTGCGCCGAGAGCAACCGGTTGCGAGAGGATGAGGCTGAGAGGAGTGTGTCATTTT	1500		
QY	841	TGCTTAACCTTAATCTGAAAGGCGCTA	867		
Db	1501	TGCTTAACCTTAATCTGAAAGGCGCTA	1527		

OY		481	AAATCTTCGTGTAATTCATTTTTAAAGTAGTGACGGTGAACCGCTGCTGCAGA	540
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OY		541	GGATGAAAAAAGGCCCTCTGATACCTCMAAGTTAGTTTCACTTTAAAGAGTCCGAG	600
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OY		601	TAAAGACGCAAGGCTTCCCGACGCGGAGAGGGCAAGTCCCTCTCATGGACGGAA	660
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OY		721	AGCCGCGAAGATCAGCTTGCGCAATCCGTGCGTGGCGGCGCTCCCTTTATAAGCCA	780
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VERSION	AR081665.1		GI:10008391	
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 981)			
TITLE	Villeponteau,B. and Harley,C.			
JOURNAL	Assays for regulators of mammalian telomerase expression			
FEATURES	Patent: US 5972605-A 2 26-Oct-1999;			
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OY		594	TGCGAAGTAAAGACGCAAGACCCTTTCCCGGACGTGGGAAAGGGCAAGTCTCTCATG	653
Db		61	TGCGAAGTAAAGACGCAAGACCCTTTCCCGGACGTGGGAAAGGGCAAGTCTCTCATG	120
OY		654	GCGGAAAATGGAATTTTATTTTCCGTTCCCGCCCAACAGCCCGCCGAGAGAGTACTC	713
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OY		714	TCAAGAGAGCGGAGAGTCAAGCTTGAGCAATCGTGGCTGGCGGCGCTCCCTTTAT	773
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Qy 834 CATTTTTGTCTAACCTTAAGGAGGCGTA 867
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Db 301 CATTTTTGTCTTAACCTTAAGGAGGCGTA 334
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OM nucleic - nucleic search, using sw model

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Title: US-09-601-267-36

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SUMMARIES

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1	108.6	12.5	76698	US-10-948-947A-1	Sequence 1, Appl
2	106	12.2	47154	US-60-659-397-12140	Sequence 12140, A
3	106	12.2	48701	PCT-US04-42189-127	Sequence 33, Appl
4	106	12.2	294575	PCT-US04-42189-85	Sequence 127, Appl
5	105	12.1	53779	US-09-543-771-6	Sequence 85, Appl
6	104.8	12.0	17570	US-10-472-963-1206	Sequence 1206, Ap
7	104.4	12.0	141540	US-10-960-414-1122	Sequence 122, App
8	104.4	12.0	142519	US-10-479-874A-9	Sequence 9, Appl
9	103.8	11.9	27069	US-11-073-360-1602	Sequence 1602, Ap
10	103.4	11.9	105001	US-60-660-817-127	Sequence 127, App
11	103.4	11.9	201	US-60-660-322-10597	Sequence 11949, A
12	102.8	11.9	19732	US-60-659-397-11949	Sequence 121, App
13	102.8	11.9	44100	US-11-028-539-63	Sequence 63, Appl
14	102.8	11.9	1799242	US-60-660-322-2215	Sequence 2215, Ap
15	102.8	11.8	80436	US-60-659-397-12235	Sequence 12235, A
16	102.4	11.8	18564	US-10-472-963-1608	Sequence 1608, Ap
17	102	11.7	457501	US-60-660-589-12	Sequence 12, Appl
18	101.6	11.7	180283	PCT-US05-10257-703	Sequence 703, Appl
19	101.4	11.7	61009	US-60-659-397-11881	Sequence 11881, A
20	101.2	11.7	61009	US-60-659-397-11881	Sequence 11881, A

21	101.2	11.7	125038	US-60-659-397-11980	Sequence 11980, A
22	101.2	11.7	166133	US-60-659-397-11887	Sequence 11887, A
23	100.8	11.6	9428	US-11-033-545-634	Sequence 634, App
24	100.6	11.6	380780	US-60-660-322-2217	Sequence 2217, App
25	100.4	11.6	99624	US-60-659-397-12123	Sequence 12123, A
26	100	11.5	38703	US-11-052-544-28	Sequence 28, Appl
27	99.8	11.5	28668	PCT-US04-42189-121	Sequence 121, Appl
28	99.6	11.5	1768	US-10-472-963-184	Sequence 184, App
29	99.6	11.5	5940	US-60-651-235-1681	Sequence 1681, Ap
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33	99.6	11.5	7044	US-60-651-235-1682	Sequence 1682, Ap
34	99.6	11.5	145616	PCT-US05-10257-222	Sequence 222, Appl
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36	99.2	11.4	150147	PCT-US05-10257-799	Sequence 799, Appl
37	99.2	11.4	221420	US-60-659-397-12132	Sequence 12132, A
38	99	11.4	26060	PCT-US05-10257-795	Sequence 795, Appl
39	98.6	11.4	48889	US-60-659-397-11973	Sequence 11973, A
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41	98.2	11.3	201	US-60-660-322-5830	Sequence 5830, Ap
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44	98	11.3	601	US-11-033-545-3591	Sequence 3591, Ap
45	98	11.3	601	US-11-033-545-10358	Sequence 10358, A

ALIGNMENTS

RESULT 1
US-10-948-947A-1/c
Sequence 1, Application US/10948947A
GENERAL INFORMATION:
APPLICANT: Monla, Brett P.
APPLICANT: Freiler, Susan M.
APPLICANT: Manoharan, Muchiah
APPLICANT: Gaarde, William A.
APPLICANT: Griffee, Richard H.
APPLICANT: Swazey, Eric B.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: ANTISENSE INHIBITION VIA RNASE H-INDEPENDENT REDUCTION IN mRNA
FILE REFERENCE: ISPH-0871
CURRENT APPLICATION NUMBER: US/10/948,947A
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: 60/392,020
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 10/461,163
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 76698
TYPE: DNA
ORGANISM: H. sapiens
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OTHER INFORMATION: antisense oligonucleotide
NAME/KEY: misc.feature
LOCATION: 15311-15410
OTHER INFORMATION: n = A,T,C or G
FEATURE:
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LOCATION: 15414
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US-10-948-947A-1
Query Match 12.5%; Score 108.6; DB 9; Length 76698;
Best Local Similarity 81.3%; Pred. No. 5.3e-15;
Matches 126; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
1 AGCTACTCAGAGAGCTGAGACGAGATCGCTTGAACCGGAGAGAGAGCTTCAGTG 60
|||||

```

Db      15588 AGCTACTGAGAGGCTGAGGAGAGGAGATGCGATGAACCAAGAGGCGGAGCTTGCAATG 15529
QY      61 AGCCGAGATCAGCGCCACTAGATCTCCATCCAGCCTGGGCGAAGAGCAAGATCCGCTCTCA 120
Db      15528 AGCCGAGATCATGCGCACTGCACTCCAAACGAGCCTGGGCGACAGAGGAGATCTGTCTCA 15469
QY      121 AAAAAAAAAATCGTTCAATTTATTTGCGATTTACT 155
Db      15468 AAAAAAAAAAAAAAAAAAAGGAGGAGGCTTAAGT 15434

```

RESULT 2

```

US-60-659-397-12140/C
; Sequence 12140, Application US/60659397
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/659,397
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12140
; LENGTH: 47154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(47154)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-659-397-12140

```

Query Match 12.2%; Score 106; DB 13; Length 47154;

Best Local Similarity 88.5%; Pred. No. 1.9e-14;

Matches 115; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```

QY      1 AGCTACTGAGAGGCTGAGAGAGGAGATGCGTTGAACCCGAGAGGAGGAGGTTGCAATG 60
Db      1099 AGCTACTGAGAGGCTGAGAGGAGGAGAGGAGATGCGATGAACCTGGAGGCGGAGCTTGCAATG 1040
QY      61 AGCCGAGATCAGCGCCACTAGATCTCCATCCAGCCTGGGCGAAGAGCAAGATCCGCTCTCA 120
Db      1039 AGCCGAGATCATGCGCACTGCACTCCAAACGAGCCTGGGCGACAGAGGAGATCTGTCTCA 980
QY      121 AAAAAAAAAA 130
Db      979 AAAAAAAAAA 970

```

RESULT 3

```

US-60-660-714-33
; Sequence 33, Application US/60660714
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: C. Frank Benneft
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Doble
; APPLICANT: Susan M. Freiler
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: COMPOSITIONS AND THEIR USES DIRECTED TO PROTEIN BINDING ACTIVITY
; FILE REFERENCE: DPK-007605.L
; CURRENT APPLICATION NUMBER: US/60/660,714
; CURRENT FILING DATE: 2005-03-10
; NUMBER OF SEQ ID NOS: 1025
; SOFTWARE: PatentSeq version 1.0
; SEQ ID NO 33
; LENGTH: 48701
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7486-7585
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: 36591-36690
; OTHER INFORMATION: n is a, c, g, or t
US-60-660-714-33

```

Query Match 12.2%; Score 106; DB 13; Length 48701;

Best Local Similarity 88.5%; Pred. No. 1.9e-14;

Matches 115; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```

QY      1 AGCTACTGAGAGGCTGAGAGAGGAGATGCGTTGAACCCGAGAGGAGGAGGTTGCAATG 60
Db      25254 AGCTACTGAGAGGCTGAGAGGAGGAGGAGATGCGTTGAACCCGAGAGGAGGAGGTTGCAATG 25313
QY      61 AGCCGAGATCAGCGCCACTAGATCTCCATCCAGCCTGGGCGAAGAGCAAGATCCGCTCTCA 120
Db      25314 AGCCGAGATCAGCGCCACTAGATCTCCATCCAGCCTGGGCGAAGAGGAGATCTCA 25373
QY      121 AAAAAAAAAA 130
Db      25374 AAAAAAAAAA 25383

```

RESULT 4

```

PCT-US04-42189-127/C
; Sequence 127, Application PC/TUS0442189
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2038
; CURRENT APPLICATION NUMBER: PCT/US04/42189
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 10/765,790
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 294575
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US04-42189-127

```

Query Match 12.2%; Score 106; DB 2; Length 294575;

Best Local Similarity 88.5%; Pred. No. 2.3e-14;

Matches 115; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```

QY      1 AGCTACTGAGAGGCTGAGAGAGGAGATGCGTTGAACCCGAGAGGAGGAGGTTGCAATG 60
Db      124842 AGCTACTGAGAGGCTGAGAGGAGGAGGAGATGCGTTGAACCCGAGAGGAGGAGGTTGCAATG 124783
QY      61 AGCCGAGATCAGCGCCACTAGATCTCCATCCAGCCTGGGCGAAGAGCAAGATCCGCTCTCA 120
Db      124782 AGTGAATCAGCGCCACTAGATCTCCATCCAGCCTGGGCGAAGAGGAGATCTCA 124723
QY      121 AAAAAAAAAA 130
Db      124722 AAAAAAAAAA 124713

```

RESULT 5

PCT-US04-42189-85
; Sequence 85, Application PC/TUS0442189
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2038
; CURRENT APPLICATION NUMBER: PCT/US04/42189
; PRIOR FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 10/765,790
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 85
; LENGTH: 53779
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-42189-85

Query Match 12.1%; Score 105; DB 2; Length 53779;
Best Local Similarity 88.4%; Pred. No. 3,3e-14;
Matches 114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 GCTACTCAGAGAGCTGAGACGAGAGATGCTTGAACCGGAGGAGGAGTTGACAGTGA 61
DB 10336 GCTACTCAGAGAGCTGCTGCGCAGAGAAATGGCTTGAACCGAGAGGAGTTGCAATA 10395
QY 62 GCCGAGATCAGCCACTAGACTCCATCCAGCCTGGCGGAGAGAGCAAGCTCCGCTCTCA 121
DB 10396 GCCGAGATCAGCTGCACTGCATCCAGCCTGAGCGAGAGAGGAGAGCTCCGCTCTCA 10455

QY 122 AAAAAAAAA 130
DB 10456 AAAAAAAAA 10464

RESULT 6
US-09-543-771-6
; Sequence 6, Application US/09543771
; GENERAL INFORMATION:
; APPLICANT: John P. Carulli et al.
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/543,771
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 62
; SEQ ID NO: 6
; LENGTH: 26928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12044), (12489), (26433), (26434), (26435), (26436), (26439), (26441)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-543-771-6

Query Match 12.1%; Score 104.8; DB 6; Length 26928;
Best Local Similarity 81.8%; Pred. No. 3.4e-14;
Matches 121; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGAGCTGAGACGAGAAATCGCTTGAACCGGAGGAGGAGTTGACAGTG 60
DB 3207 AGCTACTCAGAGAGCTGAGGAGAGAAATGGCTGAACCTGGAGGCGGAGCTTGACAGTG 3266
QY 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCTGGCGGAGAGAGCAAGACTCCGCTTCA 120
DB 3267 AGCCGAGATTCGGCCACTGCACTCCATCCAGCCTGGGCGAGAGATTAGATCCGCTCTCA 3326
QY 121 AAAAAAAAAATCGTACATTTATGCTG 148
DB 3327 AAAAAAAAAAAAAAAAAAATTAGCTG 3354

RESULT 7
US-10-472-963-1206/c
; Sequence 1206, Application US/10472963
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5954PCT
; CURRENT APPLICATION NUMBER: US/10/472,963
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/US02/09370
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1834
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1206
; LENGTH: 17570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-472-963-1206

Query Match 12.0%; Score 104.4; DB 9; Length 17570;
Best Local Similarity 87.7%; Pred. No. 4e-14;
Matches 114; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGAGCTGAGACGAGAAATCGCTTGAACCGGAGGAGGAGTTGACAGTG 60
DB 4158 AGCTACTCAGAGAGCTTGAAGGAGAAATGGCATAAACCGAGAGGAGCTTGACAGTG 4099
QY 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCTGGCGGAGAGAGCAAGACTCCGCTTCA 120
DB 4098 AGCCGAGATTCGGCCACTGCACTCCATCCAGCCTGGGAGAGAGGAGAGACTCCGCTTCA 4039
QY 121 AAAAAAAAA 130
DB 4038 AAAAAAAAA 4029

RESULT 8
US-10-960-414-122
; Sequence 122, Application US/10960414
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSHY
; APPLICANT: VEGA, VINSENUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 122
; LENGTH: 141540
; TYPE: DNA
; ORGANISM: Homo sapiens

US-60-660-322-10597

```
; Sequence 10597, Application US/60660322
; GENERAL INFORMATION:
; APPLICANT: LUKE, May et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001572
; CURRENT APPLICATION NUMBER: US/60/660,322
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 28070
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10597
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-660-322-10597
```

```
Query Match 11.9%; Score 102.8; DB 13; Length 201;
Best Local Similarity 82.9%; Pred. No. 5.7e-14;
Matches 116; Conservative 1; Mismatches 23; Indels 0; Gaps 0;
```

```
QY 1 AGCTACTCAGAGGCTGAGACACAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
DB 25 AGCTACTTGGGAGGCTGAGCGCGAGAAATGCGTGAACCCGGAGGACAGAGCTTGTAGTG 84
QY 61 AGCCGAGATCAGCGCACTAGACTCCATCCAGGCTGGGCGAAAGAGCAAGACTCCGCTTCA 120
DB 85 AGCCGAGATCAGCGCAATGAACTCCATCCAGGCTGAGCGAGAGAGAGACTCGGCTTCA 144
QY 121 AAAAAAAAAAATCGTTACAAT 140
DB 145 AAAAAAAAAAAAAAAAAAAT 164
```

```
RESULT 13
US-60-659-397-11949/C
; Sequence 11949, Application US/60659397
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/659,397
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11949
; LENGTH: 19732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-659-397-11949
```

```
Query Match 11.9%; Score 102.8; DB 13; Length 19732;
Best Local Similarity 86.9%; Pred. No. 9.1e-14;
Matches 113; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 1 AGTACTCAGAGGCTGAGACACAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
DB 15909 AGTACTCGGAGGCTGAAGGAGGAGAAATCGCTTGAACCCGGAGGACAGAGTTGTAGTG 15850
QY 61 AGCCGAGATCAGCGCACTAGACTCCATCCAGGCTGGGCGAAAGAGCAAGACTCCGCTTCA 120
DB 15849 AGCCGAGATGAGCTGACACTCCATCCAGCTAGTGACAGAGCAAGACTCTGTCTCA 15790
QY 121 AAAAAAAAAA 130
DB 15789 AAAAAAAAAA 15780
```

RESULT 14

```
US-11-028-539-63
; Sequence 63, Application US/11028539
; GENERAL INFORMATION:
; APPLICANT: ALLIEL, Patrick
; APPLICANT: PERIN, Jean-Pierre
; APPLICANT: RIEGER, Francois
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND DECODED PROTEIN SEQUENCE FAMILY WITH HL
; TITLE OF INVENTION: ENDOGENOUS RETROVIRAL MOTIFS
; FILE REFERENCE: 200936US0PCT
; CURRENT APPLICATION NUMBER: US/11/028,539
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: US/09/719,554
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: PCT/FR99/01513
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 44100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-028-539-63
```

```
Query Match 11.9%; Score 102.8; DB 11; Length 44100;
Best Local Similarity 86.9%; Pred. No. 9.9e-14;
Matches 113; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 1 AGTACTCAGAGGCTGAGACACAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
DB 40085 AGTACTTGGGAGGCTGAGACAGAGAAATGCTTGAACCCGAGAGGTGAGGTTGCAGTG 40144
QY 61 AGCCGAGATCAGCGCACTAGACTCCATCCAGGCTGGGCGAAAGAGCAAGACTCCGCTTCA 120
DB 40145 AGCCGAGATGACCACTGCACTCCATCCAGGCTGGGCGAACAGAGCAAGACTGTGTCTCA 40204
QY 121 AAAAAAAAAA 130
DB 40205 AAAAAAAAAA 40214
```

```
RESULT 15
US-60-660-322-2216
; Sequence 2216, Application US/60660322
; GENERAL INFORMATION:
; APPLICANT: LUKE, May et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001572
; CURRENT APPLICATION NUMBER: US/60/660,322
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 28070
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2216
; LENGTH: 1790242
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (1790242)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-660-322-2216
```

```
Query Match 11.9%; Score 102.8; DB 13; Length 1790242;
Best Local Similarity 82.9%; Pred. No. 1.5e-13;
Matches 116; Conservative 1; Mismatches 23; Indels 0; Gaps 0;
```

```
QY 1 AGTACTCAGAGGCTGAGACACAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
DB 1209396 AGTACTTGGGAGGCTGAGCGGAGAAATGCGTGAACCCGGAGGACAGAGCTTGTAGTG 1209455
QY 61 AGCCGAGATCAGCGCACTAGACTCCATCCAGGCTGGGCGAAAGAGCAAGACTCCGCTTCA 120
```

Wed Apr 27 17:43:12 2005

us-09-601-267-36.inpn

Page 6

DB 1209456 ACCGAGATCAAGCCAMTGAATCACTCCAGGCTGAGCGACAGAGGAGACTCGGTCTCA 1209515

OY 121 AAAAAAAAAATGTTACAT 140
|||||

DB 1209516 AAAAAAAAAAAAAAAAAAT 1209535
|||||

Search completed: April 26, 2005, 22:37:32
Job time : 467.827 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:33 ; Search time 2673.73 Seconds
(without alignments)
8940.469 Million cell updates/sec

Title: US-09-601-267-37

Perfect score: 628

Sequence: 1 tctgacctgactacagac.....tctcgtcgtactccagcg 628

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb.est1:*
2: gb.est2:*
3: gb.hic:*
4: gb.est3:*
5: gb.est4:*
6: gb.est5:*
7: gb.est6:*
8: gb.gsa1:*
9: gb.gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	12.6	2876	3	AK085092 Mus muscu
2	76	12.1	624	2	BB660202 BB660202
3	61.8	9.8	286	6	CB937393 IPCCX13
4	61.2	9.7	290	9	CR139916 Reverse s
5	58.8	9.4	729	9	AG451206 Mus muscu
6	58.2	9.3	323	5	BU551516 AGENCOURT
7	58.2	9.3	743	9	AG612453 Mus muscu
8	58.2	9.3	1281	9	AG349913 Mus muscu
9	57.8	9.2	735	9	AG458145 Mus muscu
10	57.8	9.2	1301	9	AG346181 Mus muscu
11	57.6	9.2	759	9	AG539897 Mus muscu
12	57.6	9.2	766	9	AG429109 Mus muscu
13	57.4	9.1	735	9	AG602238 Mus muscu
14	57.4	9.1	802	9	AG604663 Mus muscu
15	57	9.1	743	9	AG591362 Mus muscu
16	57	9.1	774	9	AG284698 Mus muscu
17	56.8	9.0	359	2	BF552926 UI-R-C2-n
18	56.8	9.0	409	1	AI072290 UI-R-C2-n
19	56.6	9.0	1101	9	CNS01537 Drosophila
20	56.4	9.0	535	9	CE837523 tigr-gsa-
21	56.2	8.9	737	9	AG530686 Mus muscu
22	56.2	8.9	772	9	AG539394 Mus muscu
23	56.2	8.9	811	9	AG567668 Mus muscu
24	56.2	8.9	1213	9	AG341273 Mus muscu

25	55.8	8.9	732	9	AG492128 Mus muscu
26	55.6	8.9	761	9	AG574939 Mus muscu
27	55.4	8.8	391	9	CE835556 tigr-gsa-
28	55.4	8.8	716	9	AG398550 Mus muscu
29	55.4	8.8	1172	9	AG324265 Mus muscu
30	55.2	8.8	786	9	AG564579 Mus muscu
31	55.2	8.8	1319	9	CL644695 CH213-79A
32	55	8.8	662	9	AG481539 Mus muscu
33	55	8.8	1456	9	AG435703 Mus muscu
34	54.8	8.7	585	4	BG928544 HNC68-1-E
35	54.8	8.7	720	9	AG280906 Mus muscu
36	54.8	8.7	782	9	AG474197 Mus muscu
37	54.8	8.7	802	9	AG459758 Mus muscu
38	54.8	8.7	1215	9	AG448698 Mus muscu
39	54.6	8.7	713	9	AG345270 Mus muscu
40	54.6	8.7	824	8	BZ258789 CH230-479
41	54.6	8.7	839	9	AG518301 Mus muscu
42	54.6	8.7	1120	9	AG332349 Mus muscu
43	54.4	8.7	741	9	AG473256 Mus muscu
44	54.4	8.7	802	9	AG484854 Mus muscu
45	54.4	8.7	1150	9	AG288203 Mus muscu

ALIGNMENTS

RESULT 1
AK085092
LOCUS
DEFINITION
AK085092.1 GI:26102453
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:DA30035J07 product:telomerase RNA component, full insert sequence.
ACCESSION
AK085092.1 GI:26102453
VERSION
AK085092.1
KEYWORDS
HTC; Cap trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., Shbata, Y., Hayatsu, N., Sugahara, Y., Shbata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2 Carninci, P., Shbata, Y., Hayatsu, N., Sugahara, Y., Shbata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159
REFERENCE
3 Shbata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Teshiro, H., Itoh, M., Suna, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, K., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
MEDLINE
11076861
PUBMED
11076861
TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE Group Phase I & II Team.
 ANALYSIS of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE (bases 1 to 2876)
 AUTHORS Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroka, T., Hirozane, T., Kuroda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Horii, F., Imorani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohgato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 FEATURES
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 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 550 ACCTAACCCGATTTTCATTAGCTGCGTGGTCTTCTTCTCCGCCGCTGTTT 609
 DB 2 ACTTAACCCGATTTTCATTAGCTGCGTGGTCTTCTTCTTCTCCGCCGCTGTTT 61
 QY 610 TCTCGCTGACTTCGACGG 628
 DB 62 TCTCGCTGACTTCGACGG 80
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 DEFINITION BB660202 RIKEN full-length enriched, 13 days embryo lung Mus
 accession BB660202
 musculus cDNA clone D430035J07 5', mRNA sequence.
 VERSION BB660202.1 GI:16494023
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 624)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwama, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipillar sequence. Genome Res. 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, K., and Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.jp) for further details.
 e mouse tissues.
 FEATURES
 source
 1. .624
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="D430035J07"
 /tissue_type="lung"
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 /db_host="DB108"
 /clone_lib="RIKEN full-length enriched, 13 days embryo lung"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'] GAGAGAGAGAGCGCGCAACTGAGTTTCTTTTCTTTTCTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGAGATTCGAGTTTAATTAATTCACCCGCCGCC 3'. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBlueScript KS(+) after bulk excision from Lambda PUC I."

ORIGIN
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/clone_lib="MSMG01 Mouse Male BAC library"

ORIGIN

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Matches 126; Conservative 0; Mismatches 113; Indels 0; Gaps 0,

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Db 51 ATTCACTTGCGCTGACTGACTCTAAATGCTGGGATTAAAGCTGTGCCACCAATCCAGC 110
Qy 189 TTCACCCCCGCGCTGGGAGTGCAGCTGGGTGAAGCGGAATTTTCTTTTCTTTT 248
Db 111 AGCAACAAATGATTTTATTAATGTTTAACTAAATAGTTTACATTTTATTAATTAAT 170
Qy 249 TTTTATAGAAAAAGGGGGGATTTGAATATCCCTACTTTCACCTAGATTAATTTCA 308
Db 171 ATTATATGGTGGGGTGGGTTAAATGCTCAAAAGCTGCTGTATGTTTCCACTGGATCA 230
Qy 309 GAAACCAAGCTCAGAGATGTCGCTGCGCTGCTGTGTGTGTATGTGTGTGTCT 367
Db 231 CATATACATGTGGCCCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 289

RESULT 8
AG349913
LOCUS
DEFINITION
Mus musculus molossinus DNA, clone:MSMG01-146P15.TU, genomic survey
sequence.
ACCESSION
AG349913
VERSION
AG349913.1 GI:47923223
KEYWORDS
GSS.
SOURCE
Mus musculus molossinus
ORGANISM
Mus musculus molossinus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC and Sequences of Library MSMg01
unpublished
2 (bases 1 to 1281)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Maabashi Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TU
LIBRARY
Vector : pBACE3.6
R.site 1 : EcoRI
R.site 2 : EcoRI.
Location/Qualifiers
1. 1281
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ORIGIN

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Oy 304 TTTCGAAGAACCAACCCACGAGATGTCGCGCCGCTGCTGCTGATATGCTGTCT 363
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 Db 245 TTTCGAGAGTAAACCTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
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 Oy 364 GTCTCAGCAGCAAGAACGATTTATTTATTTATTTATTTATTTATTTATTT 416
 |||||
 Db 305 GTGTNNNNNNNNNNNNNTTNTNTNTTTTNTTTTNTTTTNTTTTNTTTT 357
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RESULT 9
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 DEFINITION Mus musculus moiossinus DNA, clone:MSMg01-345E14.T7, genomic survey
 sequence.
 ACCESSION AG458145
 VERSION AG458145.1 GI:48149659
 KEYWORDS GSS.
 SOURCE Mus musculus moiossinus
 ORGANISM Mus musculus moiossinus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 BAC end Sequences of Library MSMg01
 JOURNAL Unpublished
 TITLE 2 (bases 1 to 735)
 REFERENCE Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 AUTHORS Direct Submission
 TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Saito-cho, Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kunya Abe (abe@rtc.riken.jp).
 Teikoku Institute, Bio Resource Center.
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp

COMMENT PRIMERS
 Sequencing : T7
 LIBRARY
 Vector : pBACe3.6
 R Site 1 : EcoRI
 R Site 2 : EcoRI.
 Location/Qualifiers
 1..735
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 /issue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

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Qy	235	TTTTTTTTTTTTTTTTTTTTT	AGTGTGAAAAAAGGGGGAA	TTGGAAATATCCCACTTCAAC	294
Db	188	TTTTTCTTTTTTATATCT	TTGTGTGACAGCTTTTTT	TGTCTTGTGTATGATTT	247
Qy	295	TCTAGTATATTTCA	AAACAAGCCTCAGAGTGTGCGTGCCTGTGTGTGTGA		354
Db	248	TATTTTCAGTTTGTGAT	CTCAGTGTATATCTGTGTGTGTGTGTGTGTGTGTG		307
Qy	355	TGTGTGTGTCTCA	CAGCAAGAAACAGATTTATATTTATTTATTTATTTATTT		414
Db	308	TGTGTGTGTGTGTGT	TT		367
Qy	415	TT	416		
Db	368	TT	369		

RESULT 10				
AC346181	AG346181	1301 bp	DNA	linear
LOCUS	Mus musculus molossinus	DNA,	clone:M5M901-141B03.TU,	GSS 02-JUN-2004
DEFINITION	sequence.			
ACCESSION	AG346181			
VERSION	AG346181.1	GI:	47919491	
KEYWORDS	GSS.			
SOURCE	Mus musculus molossinus			
ORGANISM	Mus musculus molossinus			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 1301)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Maashita Hattori, The Institute of Physical
and Chemical Sciences, National Institute of Advanced Industrial
Science and Technology (AIST) (ISC)

COMMENT

```

Tsukuba Institute, 8-1-3 Asaka, Maebashi City,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TV
LIBRARY
vector : pBACe3.6
R.Site 1 : EcORI
R.Site 2 : EcORI.
Location/Qualifiers
1..1301
FEATURES
source

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ORIGIN

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312 ACCAAGCCTGAGATGTGTGGCTGCCTGCTGTGTGTGTGTATGTGTGTGTCTTCAACA 371

Oy

D6 ACAATCCACAGCTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTNN 285
Dy GCAAGAAACAGTTTTATTATTATTATTATTATTATTATT 416
Db NNNTNNNNNTTTTTTTTTTTTTTTTTTTTTTTTTT 330

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LOCUS	759 bp DNA linear GSS 05-JUN-2004	
DEFINITION	Mus musculus molossinus DNA, clone:Msmg01-452L08.TJ, genomic survey	
ACCESSION	AGS39897	
VERSION	AGS39897	
KEYWORDS	GSS.	
SOURCE	AGS39897.1 GI:48300311	
ORGANISM	GSS.	
	Mus musculus molossinus	
	Mus musculus molossinus	

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC and Sequences of Library MSW01
Unpublished
2 (bases 1 to 759)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Maehara Hattori, The Institute of Physical
and Chemical Sciences, National Institute of Advanced Industrial Science and Technology (AIST)

COMMENT

```

Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rcc.riken.jp
PRIMERS
Sequencing : TU
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : BcoRI.
Location/Qualifiers
1..759
FEATURES
source

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ORIGIN

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Qy	403	TTTATTTATTTTTTT 416	
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sequence.
ACCESSION AG429109
VERSION AG429109.1 GI:48072172
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
REFERENCE
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
2 (bases 1 to 766)
REFERENCE Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
AUTHORS Direct Submission
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
JOURNAL and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kunya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : BclRI
FEATURES
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QY 347 TGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTATTTATTTATTTA 406
DB 213 TGTGTATG 272
QY 407 TTTATTTTGTG 417
DB 273 TTTTNTCTTG 283
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DEFINITION Mus musculus molossinus DNA, clone:MSMg01-534J10.T7, genomic survey
sequence.
ACCESSION AG602238
VERSION AG602238.1 GI:48363068

KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
REFERENCE
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
2 (bases 1 to 735)
REFERENCE Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
AUTHORS Direct Submission
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
JOURNAL and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kunya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : BclRI
FEATURES
source
Location/Qualifiers
1..735
/organism="Mus musculus molossinus"
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/sex="male"
/issue_type="mixture of kidney and spleen"
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Matches 97; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 237 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 296
DB 269 TTGGGTTTATATGACCTAGACAAATATCTTCATCTTACATCTTCTGACACG 328
QY 297 TGTATATTTTCAAGAAACCAAGCTCAGAGATGCGCGTGCGTGCTGTGTATG 356
DB 329 GAACACTTTTCAAGAAATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 388
QY 357 TG 416
DB 389 TG 448
RESULT 14
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DEFINITION Mus musculus molossinus DNA, clone:MSMg01-537M08.TU, genomic survey
sequence.
ACCESSION AG604663
VERSION AG604663.1 GI:48365493
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
REFERENCE
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 26, 2005, 15:59:17 ; Search time 430.989 Seconds
(without alignment)
8625.744 Million cell updates/sec

Title: US-09-601-267-37

Perfect score: 628
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 40 summaries

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2: geneeqn19908:*
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4: geneeqn20018:*
5: geneeqn20028:*
6: geneeqn20038:*
7: geneeqn20048:*
8: geneeqn20058:*
9: geneeqn20068:*
10: geneeqn20078:*
11: geneeqn20088:*
12: geneeqn20098:*
13: geneeqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	628	100.0	628	AAZ07249	Aaz07249 Mouse tel
2	628	100.0	4044	AAZ07248	Aaz07248 Mouse tel
3	575.8	91.7	622	AAZ07322	Aaz07322 Mouse tel
4	344.4	54.8	1259	AAZ07322	Aaz07322 Mouse tel
5	137	21.6	560	AAZ07322	Aaz07322 Mouse tel
6	135.4	21.6	534	AAZ07322	Aaz07322 Mouse tel
7	79	12.6	397	AAZ07322	Aaz07322 Mouse tel
8	71.8	11.4	568	AAZ07322	Aaz07322 Mouse tel
9	65.8	10.5	552	AAZ07322	Aaz07322 Mouse tel
10	60.2	9.6	6731	AAZ07322	Aaz07322 Mouse tel
11	60.2	9.6	6731	AAZ07322	Aaz07322 Mouse tel
12	60.2	9.6	6731	AAZ07322	Aaz07322 Mouse tel
13	55.2	8.8	7135	AAZ07322	Aaz07322 Mouse tel
14	54.6	8.7	599	AAZ07322	Aaz07322 Mouse tel
15	54.6	8.7	599	AAZ07322	Aaz07322 Mouse tel
16	54.6	8.7	599	AAZ07322	Aaz07322 Mouse tel
17	54.4	8.7	171324	AAZ07322	Aaz07322 Mouse tel
18	54	8.6	6988	AAZ07322	Aaz07322 Mouse tel
19	52.8	8.4	11691	AAZ07322	Aaz07322 Mouse tel
20	52.6	8.4	6306	AAZ07322	Aaz07322 Mouse tel

21	52.4	8.3	8961	6	ABK28428
22	52.4	8.3	8961	6	ABK28428
23	52.4	8.3	219352	13	ABD33098
24	52.2	8.3	85341	13	ABD32883
25	52	8.3	7304	5	ABA17950
26	52	8.3	7306	5	ABA17949
27	52	8.3	9177	5	ABA17951
28	51.8	8.2	7104	6	ABK70395
29	51.8	8.2	7104	6	ABK70395
30	51.8	8.2	7104	6	ABK70395
31	51.6	8.2	433	4	AAI87368
32	51.4	8.2	224112	13	ABD32600
33	51.2	8.2	256294	13	ABD33020
34	51	8.1	5044	6	ABK32840
35	51	8.1	15782	6	ABK28135
36	50.8	8.1	17594	6	ABK34027
37	50.8	8.1	231222	10	ADL13693
38	50.6	8.1	42104	11	ACN44606
39	50.4	8.0	415	4	AAI85215
40	50.4	8.0	2960	4	ABK05844
41	50.4	8.0	5274	12	ADQ25455
42	50.4	8.0	9950	8	ABK17768
43	50.4	8.0	48853	13	ABD33472
44	50.4	8.0	110000	10	ABQ84281_3
45	50.2	8.0	2983	4	AAK83652

ALIGNMENTS

RESULT 1	AAZ07249	AAZ07249 standard; DNA; 628 BP.
XX	AAZ07249;	
XX	22-OCT-1999	(first entry)
XX	Mouse telomerase RNA gene (terc) 5' flanking region.	
XX	Telomerase RNA; TR; promoter; cytochrome; cancer; neoplasia; terc;	
XX	gene therapy; thymidine kinase gene; anticancer therapy; mouse; ss.	
XX	Mus sp.	
XX	WO9318964-A2.	
XX	05-AUG-1999.	
XX	29-JAN-1999;	99WO-GB000308.
XX	29-JAN-1998;	98GB-00001902.
XX	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.	
XX	Keith W;	
XX	WPI; 1999-479183/40.	
XX	Mouse and human telomerase RNA gene promoters, useful for tumor specific gene therapy.	
XX	Claim 9; Fig 4b; 10pp; English.	
XX	The invention relates to promoter regions from mouse and human telomerase RNA (TR) component genes. The TR gene promoter can be linked to a heterologous gene, especially a gene encoding a cytochrome, for therapy of cancer, especially neoplasia. The telomerase is necessary for the unrestricted proliferative capacity of many human cancers. Mutation or dysregulation of the telomerase repression pathway may cause reactivation or upregulation of telomerase expression in cancer. Substances, identified in the methods, can be used to block transcription from the TR gene promoter through interaction of the 5' regulatory sequences. These	

CC substances, e.g. antisense oligonucleotides, transcription factors,
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially p67s2-codapp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents a mouse TR gene (terc) 5'
CC flanking sequence
CC

XX Sequence 628 BP; 129 A; 137 C; 160 G; 202 T; 0 U; 0 Other;

Query Match 100.0%; Score 628; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGACCTTGAACCTAGACAGCTCTGCTCAGCCTCTCAAGCTGGATTATAGGCTCG 60
DB 1 TGTGACCTTGAACCTAGACAGCTCTGCTCAGCCTCTCAAGCTGGATTATAGGCTCG 60
QY 61 GGTGACCTTGAACCTTGAATCTTTTCTTGTGAACTCAGTACCTGTTGGCCATCAGT 120
DB 61 GGTGACCTTGAACCTTGAATCTTTTCTTGTGAACTCAGTACCTGTTGGCCATCAGT 120
QY 121 CACAAGAGATCCCGCTGCTCTGCTCTCAATTTCTGGAATTAAGATTGGCCACTT 180
DB 121 CACAAGAGATCCCGCTGCTCTGCTCTCAATTTCTGGAATTAAGATTGGCCACTT 180
QY 181 TTCCCACTTCAACCCCGGCTGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
DB 181 TTCCCACTTCAACCCCGGCTGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
QY 241 TTTTCTTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
DB 241 TTTTCTTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
QY 301 ATATTTCAGAAACCAAGCTCAGAGATGCGCGTGTGCTGTGCTGTGCTGTGCTGTG 360
DB 301 ATATTTCAGAAACCAAGCTCAGAGATGCGCGTGTGCTGTGCTGTGCTGTGCTGTG 360
QY 361 TGTGCTCAGAGCAAGAAACAGATTATTTATTTATTTATTTATTTATTTATTTGCA 420
DB 361 TGTGCTCAGAGCAAGAAACAGATTATTTATTTATTTATTTATTTATTTATTTGCA 420
QY 421 GTGACTGGCTAGAGAAAGTGGGAGACGGGAGCAAAATGGGAGAGAGACATTTCCG 480
DB 421 GTGACTGGCTAGAGAAAGTGGGAGACGGGAGCAAAATGGGAGAGAGACATTTCCG 480
QY 481 CAAAGTCTGGGCTCGACCAATCGCGGCCATGAGGATATTTAAGGTGAGAGGCGGCTA 540
DB 481 CAAAGTCTGGGCTCGACCAATCGCGGCCATGAGGATATTTAAGGTGAGAGGCGGCTA 540
QY 541 GGGCTTGGGCACTTAACCTGATTTTCAATTAGCTGTGGTCTGTGCTTTTCTCCGCC 600
DB 541 GGGCTTGGGCACTTAACCTGATTTTCAATTAGCTGTGGTCTGTGCTTTTCTCCGCC 600
QY 601 CGCTGTTTTCTCGCTGACTTCCAGGG 628
DB 601 CGCTGTTTTCTCGCTGACTTCCAGGG 628

RESULT 2
AAZ07248
ID AAZ07248 standard; DNA; 4044 BP.

XX AAZ07248;

XX 22-OCT-1999 (first entry)

XX Mouse telomerase RNA gene (terc) sequence.

KW Telomerase RNA; TR; promoter; cytoxin; cancer; neoplasia; terc;
KW gene therapy; thymidine kinase gene; anticancer therapy; mouse; ss.
OS Mus sp.
XX MO9938964-A2.
XX
XX 05-AUG-1999.
XX
XX 29-JAN-1999; 99WO-GB000308.
XX
XX 29-JAN-1998; 98GB-00001902.
XX
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Keich WN;
XX WPI; 1999-479183/40.
XX
XX Mouse and human telomerase RNA gene promoters, useful for tumor specific
XX gene therapy.
XX
XX Disclosure; Fig 2; 109pb; English.

CC The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytoxin, for therapy of
CC cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors,
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially p67s2-codapp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents a mouse TR gene (terc) sequence
CC

XX Sequence 4044 BP; 1023 A; 928 C; 973 G; 1120 T; 0 U; 0 Other;

Query Match 100.0%; Score 628; DB 2; Length 4044;
Best Local Similarity 100.0%; Pred. No. 2.1e-144;
Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGACCTTGAACCTAGACAGCTCTGCTCAGCCTCTCAAGCTGGATTATAGGCTCG 60
DB 1010 TGTGACCTTGAACCTAGACAGCTCTGCTCAGCCTCTCAAGCTGGATTATAGGCTCG 1069
QY 61 GGTGACCTTGAACCTTGAATCTTTTCTTGTGAACTCAGTACCTGTTGGCCATCAGT 120
DB 1070 GGTGACCTTGAACCTTGAATCTTTTCTTGTGAACTCAGTACCTGTTGGCCATCAGT 1129
QY 121 CACAAGAGATCCCGCTGCTCTGCTCTCAATTTCTGGAATTAAGATTGGCCACTT 180
DB 1130 CACAAGAGATCCCGCTGCTCTGCTCTCAATTTCTGGAATTAAGATTGGCCACTT 1189
QY 181 TTCCCACTTCAACCCCGGCTGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
DB 1190 TTCCCACTTCAACCCCGGCTGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1249
QY 241 TTTTCTTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300
DB 1250 TTTTCTTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1309
QY 301 ATATTTCAGAAACCAAGCTCAGAGATGCGCGTGTGCTGTGCTGTGCTGTGCTGTG 360
DB 1310 ATATTTCAGAAACCAAGCTCAGAGATGCGCGTGTGCTGTGCTGTGCTGTGCTGTG 1369

XX PD 25-JAN-1996.
 XX PF 07-JUL-1995; 95WO-US008620.
 XX PR 07-JUL-1994; 94US-00272102.
 PR 27-OCT-1994; 94US-00330123.
 PR 13-FEB-1995; 95US-00387524.
 PR 07-JUN-1995; 95US-00485778.
 XX PA (COLD-) COLD SPRING HARBOR LAB.
 XX PA (GERO-) GERON CORP.
 PI Andrews WH, Avillion AA, Feng J, Funk W, Greider C, Marhunda MA;
 PI Villeponteau B;
 XX WPI; 1996-097428/10.
 XX DR RNA components of (non)human mammalian telomerase(s) - useful in studying
 PT cell senescence and immortalisation.
 XX PS Claim 11; Fig 3; 85pp; English.
 CC The RNA components of (non) human mammalian telomerase(s) especially from
 CC mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the telomerase;
 CC probes and primers can be used in detection; vectors and host cells
 CC transformed with the isolated telomerase genes can be used for production
 CC of telomerases; RNA and DNA ribozymes and triplex forming
 CC oligonucleotides directed against the telomerase genes can be used
 CC therapeutically as can plasmids. A mouse which lacks the telomerase gene
 CC (also claimed) can be used for study of telomere regulation in vivo, and
 CC the role it plays in immortalisation. This DNA sequence encodes the mouse
 CC telomerase RNA component
 XX SQ Sequence 1259 BP; 265 A; 312 C; 369 G; 313 T; 0 U; 0 Other;

Query Match 54.8%; Score 344.4; DB 2; Length 1259;
 Best Local Similarity 99.7%; Pred. No. 9.9e-75;
 Matches 345; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 CCTACTTCAACTGATATATTTGAGAAACCAAGCCTGAGATGCGTGCCTG 342
 DB 323 CCTACTTCAACTGATATATTTGAGAAACCAAGCCTGAGATGCGTGCCTG 382

QY 343 TGTGTGTGTATGTGTGTGTCTCAAGCAAGAAACGATTTTATTTTATTTT 402
 DB 383 TGTGTGTGTATGTGTGTGTCTCAAGCAAGAAACGATTTTATTTTATTTT 442

QY 403 TTTATTTATTTTGTGAAGTACTGAGTGGGGAAGGCGGAGCAATGGG 462
 DB 443 TTTATTTATTTTGTGAAGTACTGAGTGGGGAAGGCGGAGCAATGGG 502

QY 463 GAAGAGGAGCATTTCCGCAAGTGTGGCTCGACCAATCAGCGCGCCATGGGAT 522
 DB 503 GAAGAGGAGCATTTCCGCAAGTGTGGCTCGACCAATCAGCGCGCCATGGGAT 562

QY 523 TAAAGTCAAGGGGCGCTAGGCTCGGCACTTAACCTGATTTTATTTAGTGTGGTCT 582
 DB 563 TAAAGTCAAGGGGCGCTAGGCTCGGCACTTAACCTGATTTTATTTAGTGTGGTCT 622

QY 583 GGTCTTTTGTCTCCGCGCGCTGTTTTCGCTGACTTCACAGCG 628
 DB 623 GGTCTTTTGTCTCCGCGCGCTGTTTTCGCTGACTTCACAGCG 668

RESULT 5
 AAT85372
 ID AAT85372 standard; DNA; 560 BP.
 AC AAT85372;
 XX DT 15-APR-1998 (first entry)
 XX DT

XX DE Mouse telomerase RNA component gene.
 XX KW Telomerase gene; transgenic organism; carcinogen; neoplastic growth;
 KW cell growth; cell senescence; mouse; ss.
 XX OS Mus sp.
 XX PN W09735967-A2.
 XX PD 02-OCT-1997.
 XX PF 21-MAR-1997; 97WO-US005070.
 XX PR 28-MAR-1996; 96US-00623166.
 XX PA (COLD-) COLD SPRING HARBOR LAB.
 XX PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX PI Greider C, Marhunda MA, Depinho RA, Lee H;
 XX WPI; 1997-489631/45.
 XX DR WPI; 1997-489631/45.
 XX PT Non-human transgenic animal not expressing endogenous telomerase - useful
 PT to test the carcinogenicity of a test compound, or to study cell growth,
 PT division or senescence.
 XX PS Disclosure; Fig 6; 58pp; English.
 CC This sequence represents the mouse telomerase RNA component gene. This
 CC sequence can be used in the transgenic organism of the invention. The
 CC organism is a non-human transgenic organism in which at least one
 CC endogenous telomerase gene encoding a telomerase component is altered and
 CC telomerase activity is altered or is not expressed. The transgenic
 CC organisms can be used as models to study telomerase activity. They can
 CC also be used as a system to test compounds suspected of being
 CC carcinogenic by exposing animals to the compound and determining
 CC neoplastic growth as an indicator of carcinogenicity. The cells and
 CC derived tissues are used to study cell growth and division and cell
 CC senescence. The organisms are able to produce cells and tissues that, in
 CC their wild type form, cannot be easily studied in vitro due to undergoing
 CC small numbers of cell divisions
 XX SQ Sequence 560 BP; 90 A; 183 C; 188 G; 99 T; 0 U; 0 Other;

Query Match 21.8%; Score 137; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 9e-24;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 CTCGACCAATCAGCGCGCCATGCGGTATTTAAGTCGAGGCGGCTAGGCTCGGAC 551
 DB 1 CTCGACCAATCAGCGCGCCATGCGGTATTTAAGTCGAGGCGGCTAGGCTCGGAC 60

QY 552 CTAACTGATTTTATTTAGTGTGGTCTGTTCTTTTGTCTCCGCCCGCTGTTTTC 611
 DB 61 CTAACTGATTTTATTTAGTGTGGTCTGTTCTTTTGTCTCCGCCCGCTGTTTTC 120

QY 612 TCGTGACTTCGAGCGG 628
 DB 121 TCGTGACTTCGAGCGG 137

RESULT 6
 AAT11025
 ID AAT11025 standard; DNA; 534 BP.
 AC AAT11025;
 XX DT 09-JUN-1996 (first entry)
 XX DT Mouse telomerase RNA component.
 DE Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
 XX KW

KM	probe; primer; ribozyme; ss.	
XX		
OS	Mus musculus.	
XX		
PN	W09601614-A2.	
XX		
PD	25-JAN-1996.	
XX		
PF	07-JUL-1995; 95WO-US008620.	
XX		
PR	07-JUL-1994; 94US-00272102.	
XX		
PR	27-OCT-1994; 94US-00330123.	
XX		
PR	13-FEB-1995; 95US-00387524.	
XX		
PR	07-JUN-1995; 95US-00485778.	
XX		
PA	(COLD-) GOLD SPRING HARBOR LAB.	
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Andrews WH, Avillion AA, Feng J, Funk W, Greider C, Marchenka MA,	
XX	Villeponteau B;	
XX		
DR	WPI; 1996-097428/10.	
XX		
PT	RNA components of (non)human mammalian telomerase(s) - useful in studying	
XX	cell senescence and immortalisation.	
PS	Claim 2; Fig 4; 85pp; English.	
XX		
CC	The RNA components of (non) human mammalian telomerase(s) especially from	
XX	mouse, rat and chinese hamster are all claimed. Antisense	
CC	oligonucleotides can be used to block the activity of the telomerase;	
XX	probes and primers can be used in detection; vectors and host cells	
CC	transformed with the isolated telomerase genes can be used for production	
XX	of telomeres; RNA and DNA ribozymes and triplex forming	
CC	oligonucleotides directed against the telomerase genes can be used	
XX	therapeutically as can plasmids. A mouse which lacks the telomerase gene	
CC	(also claimed) can be used for study of telomere regulation in vivo, and	
XX	the role it plays in immortalisation. This is the mouse telomerase RNA	
CC	component	
XX		
SO	Sequence 534 BP; 84 A; 169 C; 184 G; 0 T; 97 U; 0 Other;	
XX		
QY	Query Match 21.6%; Score 135.4; DB 2; Length 534;	
XX	Best Local Similarity 69.3%; Pred. No. 2.2e-23;	
QY	Matches 95; Conservative 41; Mismatches 1; Indels 0; Gaps 0	
DB	492 CTGGACCAATCAGCGCGCGCATGGGTATTTAAGGTCCAGAGGCGGCTAGGCGCTCGGCAC 551	
XX	1 CUCGACCAUUCAGCGCGGACCAUUGGGGUUUAAGGUCAGAGGCGGCGUAGGCCUCGCGAC 60	
QY	552 CTAAACCTGATTTTCATTAGCTGTGTGGTCTCTGTTCTCCGCCGCTGTTTTC 611	
DB	61 CUAACCCUGAUUUUAUUAUGGUGGUGUUCUGUCUUUUGUUCUCCGCCGCGUUUUUC 120	
QY	612 TCGCTGACTTCAGCGG 628	
DB	121 UCGCUGACUUCACGCGG 137	
RESULT 7		
ID	ADT86993	
XX	ADT86993 standard; DNA; 397 BP.	
XX		
AC	ADT86993;	
XX		
DT	16-DEC-2004 (first entry)	
XX		
DE	Mouse telomerase RNA (TER) derived DNA.	
XX		
ds:	snRNA; small nuclear RNA; box HACA; mRNA splicing; mRNA processing;	
KM	rRNA processing; RNA methylation site selection; pseudouridine formation;	
XX	HACA-snoRNA; telomerase RNA; cancer; tumour; cell proliferation;	
KM	cytomegaloma infection; RNA-mediated degradation; 26556; neo gene; siRNA;	

XX	small interfering RNA; telomerase RNA; TER; mouse; selection marker.
OS	Mus musculus.
XX	WO2004069148-A2.
XX	19-AUG-2004.
PD	
XX	
PF	04-FEB-2004; 2004WO-IL000108.
XX	
PR	04-FEB-2003; 2003US-0444670P.
XX	
PA	(UYBA-) UNIV BAK-ILAN.
P1	Michaeli S;
DR	WPI; 2004-604326/58.
XX	
PT	New isolated small nuclear RNA (snRNA) polynucleotides, useful for
XX	inducing RNA-mediated degradation of snRNA or for treating diseases
PT	associated with activity of small nuclear RNA, e.g. cancer.
XX	
PS	Disclosure; SEQ ID NO 40; 79pp; English.
XX	
CC	The present invention provides the method for downregulating snRNA
CC	(small nuclear RNA) molecules or the box H/ACA containing RNA molecules.
CC	The method can be used to treat the diseases associated with the activity
CC	of small nuclear RNA. Small nuclear RNA molecules are the important
CC	regulators of gene expression. They participate in mRNA splicing, mRNA
CC	and RNA processing, RNA methylation site selection and pseudouridine
CC	formation (box H/ACA-snRNA). The telomerase RNA is an important nuclear
CC	RNA which serves as a template for telomerase replication. It contains
CC	box H/ACA like domain which confers the functional localisation of this
CC	RNA to the nucleus. The majority of the cancerous tumours contain active
CC	telomerase which contributes to cell proliferation. It has been found
CC	that the trypanosome infection is associated with the parasite's snRNA
CC	expression. The polynucleotides of the invention are useful for inducing
CC	RNA-mediated degradation of a small nuclear RNA. They are useful for
CC	down regulating snRNA molecules or box H/ACA-containing RNA molecules.
CC	The telomerase activity of the cancer cells can be inhibited by a
CC	polynucleotide sequence which is capable of inducing RNA mediated
CC	degradation of the human telomerase RNA. The snRNA-2 was found to be
CC	part of a gene cluster which includes two additional coding sequences of
CC	novel RNA termed as h2 and h3. It has also observed that the snRNA-2
CC	silencing occurs at the mature RNA transcript level and snRNA silencing
CC	results in decreased snRNA-2 guided methylation on the 5.8rRNA. The
CC	expression level of the snRNA-2 transcripts depend on the orientation of
CC	the snRNA-2 gene with respect to neo gene (selection marker). It has
CC	also found that the silencing of sno-RNA-2 is mediated through the
CC	production of siRNA (small interfering RNA) which can produce in both
CC	nucleus and cytoplasm. The invention suggests that the siRNA mediated
CC	snRNA-2 silencing is not unique to snRNA cluster-2. It is also
CC	applicable for mammalian snRNAs. The proposed nucleic acid construct
CC	comprises of a selection marker gene in reverse orientation. It also
CC	includes two promoters and each promoter is capable of directing the
CC	transcription of a specific strand of the nucleotide. The presented
CC	nucleotide sequence is the mouse telomerase RNA (TER) derived DNA.
XX	
SQ	Sequence 397 BP; 59 A; 136 C; 129 G; 73 T; 0 U; 0 Other;
Query Match	12.6%; Score 79; DB 13; Length 397;
Best Local Similarity	100.0%; Pred. No. 1.5e-09;
Matches	79; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	550 ACCTAACCCGTGATTTTCATGAGCTGTGGCTTCGCTTTTGTCGCCGCCGCTGTTT 609
DB	1 ACCTAACCCGTGATTTTCATGAGCTGTGGCTTCGCTTTTGTCGCCGCCGCTGTTT 60
QY	610 TCTCGCTGACTTCAGCGG 628
DB	61 TCTCGCTGACTTCAGCGG 79

```
RESULT 8
AAT11030
ID AAT11030 standard; DNA; 568 BP.
XX
AC AAT11030;
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the rat telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
KW probe; primer; ribozyme; ss.
XX
OS Rattus rattus.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US008620.
XX
PR 07-JUL-1994; 94US-00272102.
PR 27-OCT-1994; 94US-00330123.
PR 13-FEB-1995; 95US-00387524.
PR 07-JUN-1995; 95US-00485778.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C, Marhunda MA;
PI Villeponteau B;
XX
DR WPI; 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in studying
PT cell senescence and immortalisation.
XX
PS Claim 36; Fig 7; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially from
CC mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the telomerase;
CC probes and primers can be used in detection; vectors and host cells
CC transformed with the isolated telomerase genes can be used for production
CC of telomerases; RNA and DNA ribozymes and triplex forming
CC oligonucleotides directed against the telomerase genes can be used
CC therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC (also claimed) can be used for study of telomere regulation in vivo, and
CC the role it plays in immortalisation. This DNA sequence encodes the rat
CC telomerase RNA component
XX
SQ Sequence 568 BP; 100 A; 160 C; 187 G; 121 T; 0 U; 0 Other;
XX
Query Match 11.4%; Score 71.8; DB 2; Length 568;
Best Local Similarity 83.2%; Pred. No. 1e-07;
Matches 94; Conservative 0; Mismatches 17; Indels 2; Gaps 1;
XX
QY 516 GGGTATTTAGGCGAGGCGGCTAGACCTCGGACCTAACCCTGATTTTCAATTAGCTGT 575
Db 51 GGGTATTTAGGCGAGGCGGCTAGACCTCGGACCTTTCGCTTAACTTATGTT--ATACCTGT 108
XX
QY 576 GGGTCTGAGTCTTTTGTCTCCGCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
Db 109 GGGTCTGAGTCTTTTGTCTCCGCCGCTGTTTTTCTCGCTGACTTCCAGCGG 161
XX
RESULT 9
AAT11029
ID AAT11029 standard; DNA; 552 BP.
XX
AC AAT11029;
XX
DT 09-JUN-1996 (first entry)
XX
```

```
XX
DE DNA encoding the chinese hamster telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
KW probe; primer; ribozyme; ss.
XX
OS Cricetus griseus.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US008620.
XX
PR 07-JUL-1994; 94US-00272102.
PR 27-OCT-1994; 94US-00330123.
PR 13-FEB-1995; 95US-00387524.
PR 07-JUN-1995; 95US-00485778.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C, Marhunda MA;
PI Villeponteau B;
XX
DR WPI; 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in studying
PT cell senescence and immortalisation.
XX
PS Claim 46; Fig 7; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially from
CC mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the telomerase;
CC probes and primers can be used in detection; vectors and host cells
CC transformed with the isolated telomerase genes can be used for production
CC of telomerases; RNA and DNA ribozymes and triplex forming
CC oligonucleotides directed against the telomerase genes can be used
CC therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC (also claimed) can be used for study of telomere regulation in vivo, and
CC the role it plays in immortalisation. This DNA sequence encodes the
CC chinese hamster telomerase RNA component
XX
SQ Sequence 552 BP; 97 A; 182 C; 184 G; 89 T; 0 U; 0 Other;
XX
Query Match 10.5%; Score 65.8; DB 2; Length 552;
Best Local Similarity 73.5%; Pred. No. 3e-06;
Matches 111; Conservative 0; Mismatches 37; Indels 3; Gaps 2;
XX
QY 480 GCAAGTGTGGGCTCTGACCAATCAAGCGCGGCA--TGGGATATTTAAGTCAGGGCGG 537
Db 1 GCGAGAGCCGCGCGCGGCTCAATCAGCGCGGCCACCCCGGATCTTAAAGGCGACTGGC 60
XX
QY 538 CTAGGCTCTGGACACCTTAACCTGATTTTCATTAGCTGTGGTCTGTTGTTCTCC 597
Db 61 GGGGCGGCTGCGACGCTTAACTTGAATTCGTAGACTGTGGTACTGTGCTTTCG-TCTCC 119
XX
QY 598 GCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
Db 120 GCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 150
XX
RESULT 10
ADS89458
ID ADS89458 standard; DNA; 6731 BP.
XX
AC ADS89458;
XX
DT 18-NOV-2004 (first entry)
XX
XX Oligonucleotide of the invention SEQ ID NO:474.
XX
```

KW	ss; cellproliferative disorder; breast; methylation; cytosstatic;
KW	gene therapy; single nucleotide polymorphism; SNP.
XX	
OS	Unidentified.
PN	WO2004035803-A2.
PD	29-APR-2004.
XX	
PF	01-OCT-2003; 2003WO-EP010881.
PR	01-OCT-2002; 2002DE-01045779.
PR	07-JAN-2003; 2003DE-0100096.
PR	17-APR-2003; 2003DE-01017955.
XX	
PA	(EPig-) EPiGENOMICS AG.
PI	Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI	Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
DR	WPt; 2004-348468/32.
XX	
PT	Predicting responsiveness of a subject with breast cell proliferative
PT	disorder, useful for treating or differentiating breast cell
PT	proliferative disorders comprises analyzing methylation pattern of a
PT	genomic DNA from the subject.
XX	
PS	Disclosure; SEQ ID NO 474; 104dp; English.
CC	The invention relates to a novel method for predicting the responsiveness
CC	of a subject with a cell proliferative disorder of the breast tissues to
CC	a therapy comprising analysing the methylation pattern of a target
CC	nucleic acid by contacting at least one of the target nucleic acids in a
CC	biological sample obtained from the subject prior to or during treatment.
CC	The method of the invention has cyostatic activity, and may have a use
CC	in gene therapy. The set of oligonucleotides comprising at least two of
CC	the oligomers are useful for detecting the cytosine methylation state
CC	and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC	method, nucleic acid, oligonucleotide, and kit are useful for the
CC	treatment, characterisation, classification and/or differentiation, of
CC	breast cell proliferative disorders. The method is also useful for
CC	predicting the responsiveness of a subject with a cell proliferative
CC	disorder of the breast tissues to a therapy. The present sequence is used
CC	in the exemplification of the invention.
XX	
SQ	Sequence 6731 BP; 2098 A; 49 C; 1358 G; 3226 T; 0 U; 0 Other;
Query Match	9.6%; Score 60.2; DB 13; Length 6731;
Best Local Similarity	57.8%; Pred. No. 0.00015;
Matches 107; Conservative	0; Mismatches 78; Indels 0; Gaps 0
OY	231 TTTTGTGTTTTTTTTTTTTTTAGTGAAAAAAGGGGGATTTGAATAATCCTACTTT 290
Dd	5456 TTATTGTTTTTTTTTTATTTATTTATTTGGAGAAGGTAATTTGGGGGTAATAATTT 551
OY	291 CAACCTAGATATTTTCAGAAACAAGCCTCAGAGATGCCTCGCTGCTGTGTGTG 350
Dd	5516 TTTTGTGTTTGAATTTTTTATATATTAATTAATTTGTGTGTGTGTGTGTGTG 557
OY	351 TGTATGCTGTGTCTCACAGCAAGAAACAATTTATTTATTTATTTATTTATTTA 410
Dd	5576 TGATGTGTGTGTATGATATAGGAGGATTTGTGTGTGTGTGTGTGTGTGTG 563
OY	411 TTTT 415
Dd	5636 TTTT 5640
RESULT 11	
ID	ADSB9732 standard; DNA; 6731 BP.
XC	ADSB9732;

[illegible]

RESULT	12
ID	ABLJ32991
XX	ABLJ32991 standard; DNA; 9731 BP.
AC	
XX	ABIJ32991;
DT	
XX	26-MAR-2002 (first entry)
DE	
XX	Human immune system associated gene SEQ ID NO: 964.
XX	
KM	Human; immune system disease; cytosine methylation; antiasclmatic;
KM	antiartherosclerotic; antianemic; cytostatic; noctropid;
KM	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KM	antiatherogenic; antiarthritis; antidiabetic; antiposoriatic;
KM	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KM	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KM	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KM	ds.
XX	
OS	Homo sapiens.
XX	
PW	WO200200928-A2.
XX	
PD	03-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP007537.
XX	
PR	30-JUN-2000; 2000DE-01032529.
PR	01-SEP-2000; 2000DE-01043826.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A. Piepenbrock C, Berlin K;
XX	
XX	WPI; 2002-130909/17.
DR	
XX	
PT	Nucleic acid comprising fragment of chemically modified gene, useful for
PT	diagnosis and treatment of diseases associated with abnormal cytosine
PT	methylation.
XX	
PS	Claim 1; SEQ ID NO 964; 32pp + Sequence Listing; German.
XX	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC	rheumatoid arthritis, psoriasis and inflammatory/digestive bowel
CC	diseases. The present sequence is a gene of the invention
XX	
SQ	Sequence 9731 BP; 3021 A; 76 C; 1991 G; 4643 T; 0 U; 0 Other;
	Query Match 9.6%; Score 60.2; DB 6; Length 9731;
	Best Local Similarity 57.8%; Fred. No. 0.00017;
	Matches 107; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY	231 TTTTTTTTTTTTTTTTTTTTGTGTAAGAAAAGGGGATTTGAATAATCCTACTTT 290
DB	5456 TTTATGTTTTTTTTTTTTTTATTATTTTGGAGAAGAGGATTTGGGGCGTAATTAATT 5515
QY	291 CAACTCTAGTATATTTTCAGAAACAAGCCTCAGAGATGCGCGTGCGTGCTGTG 350
DB	5516 TTTTGTGTTGTAATTTTTTATATATATTTAATTTGTGTGTGTGTGTGTGTG 5575
QY	351 TGATGTGTGTGTGTCACAGCAAGAAACAGATTTATATATTTTATTTATTTATTTA 410
DB	5576 TGTGTGTGTGTGTGTATGATAGAGGAGTTGTGTGTATAGATGTGTTTTTTTTTGA 5638
QY	411 TTTTT 415
DB	5636 TTTT 5640

RESULT 13
 AAS46424
 ID AAS46424 standard; DNA; 7135 BP.
 XX
 AC AAS46424;
 XX
 DT 18-DEC-2001 (first entry)
 DE Tumour suppressor gene derived chemically modified sequence #146.
 XX
 KM Human; tumour suppressor gene; oncogene; antitumour; cyrostatic; cancer;
 KM tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KM cytosine methylation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200168912-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-EP002955.
 XX
 PR 15-MAR-2000; 2000DE-01013847.
 PR 06-APR-2000; 2000DE-01019058.
 PR 07-APR-2000; 2000DE-01019173.
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-602752/68.
 XX
 PT Fragments of chemically modified genes associated with tumor suppressor
 PT genes and oncogenes, useful in designing primers and probes for analyzing
 PT diseases associated with cytosine methylation state e.g. cancer.
 XX
 PS Claim 1; SEQ ID NO 146; 27pb; English.
 XX
 CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and oncogenes
 CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
 CC 500 are missing from the sequence listing) sequences (Ss) and sequences
 CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
 CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
 CC probes for detecting the cytosine methylation state and/or single
 CC nucleotide polymorphisms and also to be used in an array for analysing
 CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
 CC probes can also be used in a method for ascertaining genetic and/or
 CC epigenetic parameters for the diagnosis and/or therapy of existing
 CC diseases or the predisposition to specific diseases, by analysing
 CC cytosine methylations. The parameters may be compared to another set of
 CC genetic and/or epigenetic parameters, the differences serving as basis
 CC for diagnosis and/or prognosis events which are disadvantageous to
 CC patients. The present sequence is one of the 533 genomic sequences
 CC derived from tumour suppressor genes and oncogenes. Sequences with even
 CC numbered Seq ID numbers are the complementary sequence of the
 CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
 CC 535, except for those whose partner sequence is missing). Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 7135 BP; 2055 A; 118 C; 1901 G; 3061 T; 0 U; 0 Other;
 XX
 Query Match 8.8%; Score 55.2; DB 4; Length 7135;
 Best Local Similarity 56.7%; Pred. No. 0.0027;
 Matches 102; Conservative 0; Mismatches 78; Indels 0; Gaps 0

Wed Apr 27 17:43:12 2005

us-09-601-267-37.rng

Page 10

Search completed: April 26, 2005, 16:28:04
Job time : 434.989 secs

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:02 ; Search time 3005.16 Seconds

(without alignments)
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Title: US-09-601-267-37

Perfect score: 628
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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GenEmbl:*
1: gb_ha:*
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4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
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11: gb_sre:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	628	100.0	628	6	BD225834 Promoter
2	628	100.0	628	6	AX019583 Sequence
3	628	100.0	4044	6	BD225799 Promoter
4	628	100.0	4044	6	AX019548 Sequence
5	628	100.0	4044	10	AF047387 Mus muscu
6	579	92.2	189715	2	AC121792 Mus muscu
7	575.8	91.7	622	6	BD225835 Promoter
8	575.8	91.7	622	6	AX019584 Sequence
9	263.6	42.0	155682	2	AC120377 Mus muscu
10	263.6	42.0	179856	2	AC119995 Mus muscu
11	172	27.4	490	10	AF221922 Mus muscu
12	168	26.8	590	10	MMU33831 U33831 Mus muscu
13	135.2	21.5	220807	2	AC139643 Rattus no
14	89.2	14.2	481	10	AF221916 Rattus no
15	79	12.6	397	10	AY058800 Mus muscu
16	77.4	12.3	397	10	AY058901 Mus spret
17	68.2	10.9	476	10	AF221928 Rattus no
18	64	10.2	212070	2	BX897694 Danio rer
19	62.4	9.9	66375	2	AC100703 Mus muscu

c 20	62.4	9.9	117773	10	AL845272	AL845272 Mouse DNA
c 21	62.2	9.9	182881	9	AC090980	AC090980 Homo sapi
c 22	62.2	9.9	183016	2	AC068611	AC068611 Homo sapi
c 23	62.2	9.9	193929	9	AC090797	AC090797 Homo sapi
c 24	62	9.9	163299	2	CR293503	CR293503 Danio rer
c 25	61.4	9.8	247684	2	BX901883	BX901883 Danio rer
c 26	60.2	9.6	6731	6	CO807024	CO807024 Sequence
c 27	60.2	9.6	6731	6	CO807298	CO807298 Sequence
c 28	60.2	9.6	9731	6	AX345893	AX345893 Sequence
c 29	59.4	9.5	188776	5	BX537130	BX537130 Zebrafish
c 30	59.4	9.5	198235	2	CR450796	CR450796 Danio rer
c 31	59.2	9.4	164356	2	AC141299	AC141299 Homo sapi
c 32	59.2	9.4	194734	2	AC083828	AC083828 Homo sapi
c 33	58.6	9.3	203294	2	CR392349	CR392349 Danio rer
c 34	58.6	9.3	235505	2	AC133422	AC133422 Rattus no
c 35	58.2	9.3	159375	5	BX005001	BX005001 Zebrafish
c 36	58	9.2	161459	2	BX927335	BX927335 Danio rer
c 37	58	9.2	181841	10	AC138792	AC138792 Mus muscu
c 38	58	9.2	218008	2	AC139438	AC139438 Rattus no
c 39	57.2	9.1	170027	2	AC110670	AC110670 Canis fam
c 40	57.2	9.1	209545	2	CR388158	CR388158 Danio rer
c 41	57.2	9.1	161519	2	AC095396	AC095396 Rattus no
c 42	57	9.1	154071	3	AC115598	AC115598 Dictyosbe
c 43	57	9.1	163325	5	AC020912	AC020912 Homo sapi
c 44	57	9.1	198776	5	BX323593	BX323593 Zebrafish
c 45	57	9.1	205827	2	AC130050	AC130050 Rattus no

ALIGNMENTS

RESULT 1	BD225834	628 bp	DNA	linear	PAT 17-UTL-2003
LOCUS	BD225834	Promoter	region of mouse and human telomerase RNA component genes.		
DEFINITION	BD225834.1	GI:33035604			
ACCESSION	BD225834				
VERSION	BD225834.1	GI:33035604			
KEYWORDS	JP 2002509699-A/37.				
SOURCE	Mus sp.				
ORGANISM	Mus sp.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.				
AUTHORS	Keith,W.N.				
TITLE	Promoter region of mouse and human telomerase RNA component genes				
JOURNAL	Patent: JP 2002509699-A 37 02-APR-2002;				
COMMENT	CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD				
	OS Mus sp. (mouse)				
	PN JP 2002509699-A/37				
	PD 02-APR-2002				
	PF 29-JAN-1999 JP 2000529424				
	PR 29-JAN-1998 GB 9801902.9				
	PI WILLIAM NICOL KEITH				
	PC				
	C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC				
	A61K48/00				
	PC A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC				
	,C12Q1/68//C12N9/12,				
	PC (A61K35/76,A61K31:522),C12N15/00,A61K37/02,C12N5/00 CC				
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	Genes				
	PH Key				
	FT source				
	FT				
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	/organism="Mus sp."				
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	Best Local Similarity				
	100.0%; Score 628; DB 6; Length 628;				
	100.0%; Pred. No. 9.1e-168;				

Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGACCTTGAACCTACAGACCTCTGCTCAGCCTCTCAACAAGCTGGATTATAGGCTCG 60
 DB 1 TGTGACCTTGAACCTACAGACCTCTGCTCAGCCTCTCAACAAGCTGGATTATAGGCTCG 60

QY 61 GGTGACCTACCTTGAATCTTTCTTTCTTGTGAACTCACTGCTGGCCATGCACT 120
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QY 121 CACAAGAGATCCGCTGCTCTGTCTCAAAATTCGAAATTAAAGATTGGCCACT 180
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QY 181 TTCCCACTTCCACCCCGGCTGTGGAGTGAAGTGGATTGAAGTTTCTTTT 240
 DB 181 TTCCCACTTCCACCCCGGCTGTGGAGTGAAGTGGATTGAAGTTTCTTTT 240

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 DB 241 TTTTCTTTTCTTTTGTGAAAAAAGGGGGGATTGGAATATCCCTACTTCAACTCTAGT 300

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 DB 301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGTGTGTGTGTGTGTGTGTGTG 360

QY 361 TGTGTCTCAGCAAGAAACAGATTTTATTTATTTTATTTTATTTTATTTTGGCA 420
 DB 361 TGTGTCTCAGCAAGAAACAGATTTTATTTATTTTATTTTATTTTATTTTGGCA 420

QY 421 GTGACTGTGCTAGAGAGATGTGGGAAAGCGGAGGACAAATGGGGAAGAGGAGCATTTCCG 480
 DB 421 GTGACTGTGCTAGAGAGATGTGGGAAAGCGGAGGACAAATGGGGAAGAGGAGCATTTCCG 480

QY 481 CAAGTCTGTGGCTCGACCAATCAGCGCGCCATGTGGGTATTTAAGTGTGAGGGCGGCTA 540
 DB 481 CAAGTCTGTGGCTCGACCAATCAGCGCGCCATGTGGGTATTTAAGTGTGAGGGCGGCTA 540

QY 541 GGCTCTGGGACCTTAACCTGATTTTCATTAGCTGTGGGTCTTGTCTTCTCCGCC 600
 DB 541 GGCTCTGGGACCTTAACCTGATTTTCATTAGCTGTGGGTCTTGTCTTCTCCGCC 600

QY 601 CGCTGTTTTCTCGCTGACTTCACGCG 628
 DB 601 CGCTGTTTTCTCGCTGACTTCACGCG 628

RESULT 2
 AX019583 628 bp DNA linear PAT 07-SEP-2000
 LOCUS AX019583 Sequence 37 from Patent WO938964.
 DEFINITION AX019583
 ACCESSION AX019583
 VERSION AX019583.1 GI:10043497
 KEYWORDS
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Keith, W.N.
 TITLE Promoter regions of the mouse and human telomerase rna component genes
 JOURNAL Patent: WO 938964-A 37 05-AUG-1999;
 KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
 FEATURES
 source location/Qualifiers
 1..628
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 /mol_type="unassigned DNA"
 /db_xref="taxon:10095"

Query Match 100.0%; Score 628; DB 6; Length 628;
 Best Local Similarity 100.0%; Pred. No. 9.1e-168;

Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGACCTTGAACCTACAGACCTCTGCTCAGCCTCTCAACAAGCTGGATTATAGGCTCG 60
 DB 1 TGTGACCTTGAACCTACAGACCTCTGCTCAGCCTCTCAACAAGCTGGATTATAGGCTCG 60

QY 61 GGTGACCTACCTTGAATCTTTCTTTCTTGTGAACTCACTGCTGGCCATGCACT 120
 DB 61 GGTGACCTACCTTGAATCTTTCTTTCTTGTGAACTCACTGCTGGCCATGCACT 120

QY 121 CACAAGAGATCCGCTGCTCTGTCTCAAAATTCGAAATTAAAGATTGGCCACT 180
 DB 121 CACAAGAGATCCGCTGCTCTGTCTCAAAATTCGAAATTAAAGATTGGCCACT 180

QY 181 TTCCCACTTCCACCCCGGCTGTGGAGTGAAGTGGATTGAAGTTTCTTTT 240
 DB 181 TTCCCACTTCCACCCCGGCTGTGGAGTGAAGTGGATTGAAGTTTCTTTT 240

QY 241 TTTTCTTTTCTTTTGTGAAAAAAGGGGGGATTGGAATATCCCTACTTCAACTCTAGT 300
 DB 241 TTTTCTTTTCTTTTGTGAAAAAAGGGGGGATTGGAATATCCCTACTTCAACTCTAGT 300

QY 301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGTGTGTGTGTGTGTGTGTGTG 360
 DB 301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGTGTGTGTGTGTGTGTGTGTG 360

QY 361 TGTGTCTCAGCAAGAAACAGATTTTATTTATTTTATTTTATTTTATTTTGGCA 420
 DB 361 TGTGTCTCAGCAAGAAACAGATTTTATTTATTTTATTTTATTTTATTTTGGCA 420

QY 421 GTGACTGTGCTAGAGAGATGTGGGAAAGCGGAGGACAAATGGGGAAGAGGAGCATTTCCG 480
 DB 421 GTGACTGTGCTAGAGAGATGTGGGAAAGCGGAGGACAAATGGGGAAGAGGAGCATTTCCG 480

QY 481 CAAGTCTGTGGCTCGACCAATCAGCGCGCCATGTGGGTATTTAAGTGTGAGGGCGGCTA 540
 DB 481 CAAGTCTGTGGCTCGACCAATCAGCGCGCCATGTGGGTATTTAAGTGTGAGGGCGGCTA 540

QY 541 GGCTCTGGGACCTTAACCTGATTTTCATTAGCTGTGGGTCTTGTCTTCTCCGCC 600
 DB 541 GGCTCTGGGACCTTAACCTGATTTTCATTAGCTGTGGGTCTTGTCTTCTCCGCC 600

QY 601 CGCTGTTTTCTCGCTGACTTCACGCG 628
 DB 601 CGCTGTTTTCTCGCTGACTTCACGCG 628

RESULT 3
 BD225799 4044 bp DNA linear PAT 17-JUN-2003
 LOCUS BD225799 Promoter region of mouse and human telomerase RNA component genes.
 DEFINITION BD225799 Promoter region of mouse and human telomerase RNA component genes.
 ACCESSION BD225799
 VERSION BD225799.1 GI:33035569
 KEYWORDS
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (Bases 1 to 4044)
 AUTHORS Keith, W.N.
 TITLE Promoter region of mouse and human telomerase RNA component genes
 JOURNAL Patent: JP 2002509699-A 2 02-APR-2002;
 CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
 COMMENT
 OS Mus sp. (mouse)
 PN JP 2002509699-A/2
 PD 02-APR-2002
 PF 29-JAN-1999 JP 2000529424
 PR 29-JAN-1998 GB 9801902.9
 PI WILLIAM NICOL KEITH
 PC
 C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC
 A61K48/00,
 PC A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC

REFERENCE	Euryarchaea; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 4044)
TITLE	Zhao,J.O., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K., Black,D.M. and Keith,W.N.
JOURNAL	Cloning and characterization of human and mouse telomerase RNA gene promoter sequences
MEDLINE	Oncogene 16 (10), 1345-1350 (1998)
REFERENCE	98206512
PUBMED	9546436
REFERENCE	2 (bases 1 to 4044)
AUTHORS	Zhao,J.O., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K., Black,D.M. and Keith,W.N.
TITLE	Direct Submission
JOURNAL	Submitted (09-FEB-1998) Medical Oncology, Beatson Institute, Switchback Rd, Glasgow G61 1BD, UK
FEATURES	Location/Qualifiers

Query Match	100.0%	Score 628	DB 10	Length 4044
Best Local Similarity	100.0%	Pred. No. 1.1e-167		
Matches 628	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	TGTCACCTTGAACATACAGACCTCCGCTCAGCTCAGCTCCCTACAAAGCTGGGATTTATAGCTCG	60
Db	1010	TGTGACCTTGAACATACAGACCTCCGCTCAGCTCAGCTCCCTACAAAGCTGGGATTTATAGCTCG	1065
QY	61	GGTCAGCTACCCCTTGAAATCTTTTTCTTTCTTGAAATCTAGTACCTGGTTGGCAGTCACT	120
Db	1070	GGTCAGCTACCCCTTGAAATCTTTTTCTTTCTTGAAATCTAGTACCTGGTTGGCAGTCACT	1122
QY	121	CACAAGAGATCCGCGCTGCTCTGTGCTCTCAAAATTCTGGAATTTAAGATTGGCGCACTT	180
Db	1130	CACAAGAGATCCGCGCTGCTCTGTGCTCTCAAAATTCTGGAATTTAAGATTGGCGCACTT	1189
QY	181	TTCCCACTTCCACCCCGCGCTGTGGAGTGGACTGGCTTGAGGTGAAATTTTTTTTTT	240
Db	1190	TTCCCACTTCCACCCCGCGCTGTGGAGTGGACTGGCTTGAGGTGAAATTTTTTTTTT	1249
QY	241	TTTTTTTTTTTTTTAGTGAAGAAAAGGGGGGATTGGAAATATCCCTACTTTCACCTTAGT	300
Db	1250	TTTTTTTTTTTTTTAGTGAAGAAAAGGGGGGATTGGAAATATCCCTACTTTCACCTTAGT	1309
QY	301	ATATTTCAAGAAACCAAGCTCAGAGATGTGGTGCTGCTGTGTGTGTGTATGTGTG	360
Db	1310	ATATTTCAAGAAACCAAGCTCAGAGATGTGGTGCTGCTGTGTGTGTGTATGTGTG	1369
QY	361	TGTGCTCAAGCAAGAAACAGATTTTATTTATTTTTTTATTTATTTATTTATTTTGGAA	420
Db	1370	TGTGCTCAAGCAAGAAACAGATTTTATTTATTTTTTTATTTATTTATTTATTTATTTTGGAA	1422
QY	421	GTCATCGGCTACAGAAAGTGGGGAAAGGGGAGCAAAATGGGGAAAGAGGAGCAATTCG	480
Db	1430	GTCATCGGCTACAGAAAGTGGGGAAAGGGGAGCAAAATGGGGAAAGAGGAGCAATTCG	1489
QY	481	CAAGTGTGGGCTTCGACCAATCAGCGCGCGCATATGGGGATTTTAAGTTCGAGGGCGGCTA	540
Db	1490	CAAGTGTGGGCTTCGACCAATCAGCGCGCGCATATGGGGATTTTAAGTTCGAGGGCGGCTA	1549
QY	541	GGCTCGGCACTTACCTGATTTTCAATTAAGCTGTGGTTCTGGTCTTTTGTCTCGGCC	600

Db	Accession	Source	Organism	Keywords	Version	Accession	Definition	Locust	Result 6
Db	1550	GGCCTCGGACACTTAACCCCTGATTTTTCATTACTGTGGTTCCTGTCCTTTGTCTCCGCC	1600						
Qy	601	CGCTGTTTCTCGCTGACTTCCAGCGG	628						
Db	1610	CGCTGTTTCTCGCTGACTTCCAGCGG	1637						
RESULT 6									
LOCUS	AC121792								
DEFINITION	AC121792	189715 bp	DNA	linear	HTG 02-SEP-2004				
ACCESSION	AC121792	21 unordered pieces.			WORKING DRAFT SEQUENCE,				
VERSION	AC121792								
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFLN.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
REFERENCE	1 (bases 1 to 189715)								
AUTHORS	Walson,R.K.								
TITLE	The sequence of Mus musculus clone								
JOURNAL	Unpublished								
REFERENCE	2 (bases 1 to 189715)								
AUTHORS	McPherson,J.D. and Waterston,R.H.								
TITLE	Direct Submission								
JOURNAL	Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park								
REFERENCE	3 (bases 1 to 189715)								
AUTHORS	Walson,R.K.								
TITLE	Direct Submission								
JOURNAL	Submitted (02-SEP-2004) Genome Sequencing Center, 4444 Forest Park								
COMMENT	On Sep 2, 2004 this sequence version replaced gi:21039881.								

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: W05SC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA040J07
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 183739 bases at least Q40
Consensus quality: 184192 bases at least Q30
Consensus quality: 184706 bases at least Q20
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1202: contig of 1202 bp in length
* 1303 1302: gap of unknown length
* 1303 2621: contig of 1319 bp in length
* 2622 2721: gap of unknown length
* 2722 4947: contig of 2226 bp in length
* 4948 5047: gap of unknown length
* 5048 6672: contig of 1625 bp in length
* 6673 6773: gap of unknown length
* 6773 8697: contig of 1925 bp in length
* 8698 8797: gap of unknown length
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* 10426 10525: gap of unknown length

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PN  JP 20025059699-A/38
PD  02-APR-2002
PF  29-JAN-1999 JP 2000529424
PR  29-JAN-1998 GB 9801902.9
PI  WILLIAM NICOL KEITH
PC
C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00,
A61K48/00,
PC A61K93/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC
,C12Q1/68/C12N9/12,
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Promoter region of mouse and human telomerase RNA component CC
Genes
FH  Key Location/Qualifiers
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Best Local Similarity	-98.1%;	Pred. No. 6.6e-153;		
Matches 617; Conservative	0;	Mismatches 2;	Indels 10;	Gaps 3

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Db	2	TGTACCTTGAACATACAGACCTCTGTGCTCAGCTCTCTACAGCTGGAAATTATAGGCTCG	61
OY	61	GCTCAGCTACCTTTGAAA-TCCTTTTCTTTCTTGGAACTCAGTACCTGGTGGCCATGCAC	119
Db	62	GGTACGCTACCTTGAATAATCTTTTCTTTCTTGGAACTCAGTACCTGGTGGCCATGCAC	121
OY	120	TCACAGAGATCCGCGCTGCTTGTCTGTCTCTCAAAATTCTGGAAATTGAACTTTGGCCACT	179
Db	122	TCACAGAGATCCGCGCTGCTTGTG----TCAAAATTCTGGAAATTGAACTTTGGCCACT	177
OY	180	TTTTCGCCACTTCCACCCCGCGCTGTGGAGTGTGACTGGGTTGAAGTGTGAAATTTTTTTTT	239
Db	178	TTTTCGCCACTTCCACCCCGCGCTGTGGAGTGTGACTGGGTTGAAGTGTGAA-----TTTT	232
OY	240	TTTTTTTTTTTTTTTTTATGTGAAAAAAGGGGGGATTTGGAAATATCCCTACTTCACTTAG	299
Db	233	TTTTTTTTTTTTTTTTTATGTGAAAAAAGGGGGGATTTGGAAATATCCCTACTTCACTTAG	292
OY	300	TATATTTCAAGAAACCAAGCTCTAGAGATGTGGTGTGGCGGTGTGTGTGTATATGT	359
Db	293	TATATTTCAAGAAACCAAGCTCTAGAGATGTGGTGTGGCGGTGTGTGTGTATATGT	352
OY	360	GTTGTGTCTCAGACAGAAACAGATTTTATTTATTTTATTTATTTATTTATTTTGGCA	419
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OY	420	AGTACGTGCTAGAGAGATGGGGAAAGCGGAGGCAAAATGGGGAAGGGAGGCAATTTCC	479
Db	413	AGTACGTGCTAGAGAGATGGGGAAAGCGGAGGCAAAATGGGGAAGGGAGGCAATTTCC	472
OY	480	GCAAGTCTGGGCTGCACCAATCAGCGCGCCCATGGGGTATTTAAGTGTGAGGGCGGCT	539
Db	473	GCAAGTCTGGGCTGCACCAATCAGCGCGCCCATGGGGTATTTAAGTGTGAGGGCGGCT	532
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Db	533	AGGCGCTCGGACCTTAACCTGTATTTTCAATATAGCTGTGGGTTCTGTGCTTTTGTTCTCCGG	592
OY	600	CGCGTGTTTTCTCGCTGACTTCCAGCGG	628
Db	593	CGCGTGTTTTCTCGCTGACTTCCAGCGG	621

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LOCUS      AX019584
DEFINITION Sequence 38 from Patent WO9328964.
ACCESSION  AX019584
VERSION     AX019584.1  GI:10043498
KEYWORDS
SOURCE
ORGANISM   Mus sp.
            Mus sp.
            Eulatyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Keith,W.N.
TITLE       Promoter regions of the mouse and human telomerase rna component
            genes
JOURNAL    Patent: WO 9328964-A 38 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES
            location/Qualifiers
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            /mol_type="unassigned DNA"
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ORIGIN

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Query Match	91.7%;	Score 575.8;	DB 6;	Length 622;
Best Local Similarity	98.1%;	Pred. No. 6.6e-153;		
Matches 617; Conservative	0;	Mismatches 2;	Indels 10;	Gaps 3;

OY		1	TGTGACCTTGGAACTACAGACCCTCGCTCAGCCCTCAAGCTCGGGATTATAGCTCG	60
Db		2	TGTGACTTTGAACATAACAACCTCGTGCTCAGCCCTCAAGCTCGGGATTATAGCTCG	61
OY		61	GGTAGGCATCCCTGGAAA-TCTTTTTCTTTTCTGGAACTCAGTACTCGTGTGCCATGCAC	119
Db		62	GGTACGCTACCTCTGAAAAATCTTTTTCTTTCTGGAACTCAGTACTCGTGTGCCATGCAC	121
OY		120	TCACAAGAAGATCCGCGCTGCTTGTGTCTCTCAAAATTCGAGATTAAAGATTGGCCCACT	179
Db		122	TCACAAGAAGATCCGCGCTGCTTGTG---TCAAAATTCGGAATTAAAGATTGGGCCACT	177
OY		180	TTTTCCCCACTTCACCCCCCGGCTGTGGGAGTGAGACTGGGTTGAAAGTGGAATTTTTTTTT	239
Db		178	TTTTCCCACCTTCACCCCCCGGCTGTGGGAGTGAGACTGGGTTGAAAGTGGA-----TTTT	232
OY		240	TTTTTTTTTTTTTTTTTAAGTAAAAAAGGGGGGATTGAAATATCCCTCATCTTCAACTCTAG	299
Db		233	TTTTTTTTTTTTTTTTTAGTAAAAAAGGGGGGATTGAAATATCCCTCATCTTCAACTCTAG	292
OY		300	TATATTTTCAGAAAACCAAGCCTCACAGATGTGTGCGGTGTGTGTGTGTGTGTGTGTGT	359
Db		293	TATATTTTCAGAAAACCAAGCCTCACAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	352
OY		360	GTGTGTCTCACAGCAAGAAAACAGATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTT	419
Db		353	GTGTGTCTCACAGCAAGAAAACAGATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTT	412
OY		420	AGTACTGTGCTAGGAAGATGGGGAGACGGGAGGACAAATGGGGAGAAAGGAGCATTTCC	479
Db		413	AGTACTGTGCTAGGAAGATGGGGAGACGGGAGGACAAATGGGGAGAAAGGAGCATTTTCC	472
OY		480	GCAAGTCTGTGGGCTTCGACCAATCAGCGCGCGCCATGGGGTATTTTAAAGTCTGAGGGCGGCT	539
Db		473	GCAAGTCTGTGGGCTTCGACCAATCAGCGCGCGCCATGGGGTATTTTAAAGTCTGAGGGCGGCT	532
OY		540	AGGCGCTCGGACCTAACCTGATTTTATTTATTTAGCTGTGTGGGTTCTGTCTTTTGTCTCGC	599
Db		533	AGGCGCTCGGACCTAACCTGATTTTATTTATTTAGCTGTGTGGGTTCTGTCTTTCTGTCTCGC	592
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RESULT 9

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LOCUS Mus musculus chromosome 3 clone RP24-262L5 map 3, *** SEQUENCING IN...
DEFINITION
AC120377 AC120377 GI:54111356
VERSION HTG; HTGS PHASE1; HTGS_FULFILL; HTGS_ACTIVEFIN.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 155682)
1 (bases 1 to 155682)
Mus musculus chromosome 3, clone RP24-262L5
Unpublished
2 (bases 1 to 155682)
Birren, B., Linton, L., Nuebaum, C., Lander, E., All, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Ginde, S., Gird, S., Goyette, M., Graham, L., Grand, P., Hager, B.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,
Landers, T., Lebeck, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Nithya, C., Norman, C. H., O'Donnell, P., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, O., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thamann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Toplam, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 155682)
Birren, B., Nuebaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,
Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
Deatellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lander, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C.,
McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thamann, N.,
Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,
Toplam, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (13-OCT-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 13, 2004 this sequence version replaced gi:53374815.
All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@broad.mit.edu
----- Project Information
Center project name: L25933
Center clone name: 262_L_5
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 110344: contig of 110344 bp in length
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* 110445 113121: contig of 2677 bp in length
* 113122 113221: gap of unknown length
* 113222 115498: contig of 2277 bp in length
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Best Local Similarity 72.9%; Pred. No. 1e-63;
Matches 468; Conservative 0; Mismatches 124; Indels 50; Gaps 8;
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DEFINITION IN PROGRESS ***, 2 ordered pieces.
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 179856)
Birren,B., Nussbaum,C. and Lander,E.
Mus musculus chromosome 3, clone RP24-120B18
2 (bases 1 to 179856)
Unpublished
Anderson,S., Barton,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,Y.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
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Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
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Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 179856)
Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Anderson,S., Arachchi,H.M., Barton,N., Bastien,V.,
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Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lu,A., Mabbitt,R.,
Maclean,C., MacDonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,T., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T., Peterson,K.,
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupbach,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.
Direct Submission

JOURNAL
COMMENT
Submitted (02-OCT-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 2, 2004 this sequence version replaced gi:51948659.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@road.mit.edu
----- Project Information
Center project name: L25880
Center clone name: 120_B_18

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 162056: contig of 162056 bp in length
* 162057 162156: gap of unknown length
* 162157 179856: contig of 17700 bp in length.
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/db_xref="taxon:10090"
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/clone="RP24-120B18"
/clone_11b="RPC1-24 Male Mouse BAC"
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Best Local Similarity 72.9%; Pred. No. 1,16-63;
Matches 468; Conservative 0; Mismatches 124; Indels 50; Gaps 8;
Qy 2 GTGACCTTGACCTACAGACCTCCGCGCTGCTTCAAGCTGGATTATAGCTCGG 61
Db 167459 GTGACCTTGACAGCGGTACCTCTGCTTCAAGCTGGATTATAGCTCGT 167400
Qy 62 GTGACCTACCTTGAAA-----TCTTTTCTTCTGGAATCACTAGT-----CTGGTT 109
Db 167399 GTGACCTACCTTGAAAATCTTTTCTTTTCTTCTGGAATCACTAGTCAAGCTG 167340
Qy 110 GGCC---ATGACATCAAGAGATCCGCTGCTTCTCTCTCAATTTCTGAATTAAA 166
Db 167339 GGCCATGATGAACATCAAGAGATCTCCAGCTTTGTCTCTCAATTTCTGGAATTAAA 167280
Qy 167 GATTGGCGCCACTTTTCCCACTTCCACCCCGGCTGTGGAGTGAAGTGGTTGAAGT 226
Db 167219 GATTGGCGCACTT-----CCCTGTGGAGTGAAGTGGTGGAGT 167237
Qy 227 GGAATTT-TTTTTTTTTTTTTTTTTTTTATGTAAGAAAAAGGGGGATGGAAATATCCCT 285
Db 167236 GGAATTTATGATGTTTAAATGAAAAAAGGGTGGGGAATGAAATATCCCT 167177
Qy 286 ACTTCAACTCTGATATTTTCAAGAAACCAAGCTCAGAAATGCTGCTGCTGCTGT 345
Db 167176 AGTTTCACGTATGATATTCAGAAACCAAGTTTCAAGAGTGTGTGTGTGTGT 167117
Qy 346 GTGTGTGTATGT 405
Db 167116 GTGCGAGT-----GCTATGACAGAAATGATTAATTAATTAATTAATTAATTAATTA 167068
Qy 406 ATTTATTTTTCAGAGT 465
Db 167067 TATTATTTATGCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 167012

QY 466 GAGGAGACATTTCCGAGAGTGTGGGCTGCAGCAATCAGCGCGGCATGAGGATTTAA 525
 DB 167011 ATRAGCAGCACTAGTGGATCTGAGACTCAGCCATCAGCGCGGCTGTGGATTTAA 166952
 QY 526 GGTGAGGAGCGGCTAGGCGCTCGGACCTTAACCTGATTTTCTAGTGTGGTCTGT 595
 DB 166951 GGGCAGCGGAGAGTGTGGCTT--GTGCTAACCTGCTTTCTTAGCTGTGATTCGT 166954
 QY 586 CTTTGTCTCCGCGCCGCTGTTTCTCGCTGACTTCAGCG 627
 DB 166893 CTTTGTCTCCGCGAGCTGTCTTCTCGCTGACTTCAGTG 166852

RESULT 11
 AF221922 490 bp DNA linear ROD 19-MAR-2000
 LOCUS AF221922 Mus musculus telomerase RNA gene, sequence.
 DEFINITION AF221922
 ACCESSION AF221922
 VERSION AF221922.1 GI:7263089
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Chen, J.L., Blasco, M.A. and Greider, C.W.
 TITLE Secondary structure of vertebrate telomerase RNA
 JOURNAL Cell 100 (5), 503-514 (2000)
 MEDLINE 20185063
 PUBMED 10721988
 REFERENCE 2 (bases 1 to 490)
 AUTHORS Chen, J.L., Blasco, M.A. and Greider, C.W.
 TITLE Direct Submission
 JOURNAL Submitted (06-JAN-2000) Molecular Biology and Genetics, Johns
 Hopkins University School of Medicine, Hunterian 617 / 725 N. Wolfe
 St., Baltimore, MD 21205, USA
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 source location/Qualifiers
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 TATA_signal 63..68
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QY 457 AATGGGAGAGGAGGACATTTCCGCAAGTGTGGGCTCGACCAATCAGCGCGCCATG 516
 DB 1 AATGGGAGAGGAGGACATTTCCGCAAGTGTGGGCTCGACCAATCAGCGCGCCATG 60
 QY 517 GGTATTTAAGTGTGAGGCGGCTAGGCGCTCGGACCTTAACCTGATTTTCTAGTGTG 576
 DB 61 GGTATTTAAGTGTGAGGCGGCTAGGCGCTCGGACCTTAACCTGATTTTCTAGTGTG 120
 QY 577 GGTTCGAGCTTTGTCTCCGCGGCTGTTTCTCGGCTGACTTCAGCG 628
 DB 121 GGTTCGAGCTTTGTCTCCGCGGCTGTTTCTCGGCTGACTTCAGCG 172

RESULT 12
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 DEFINITION U33831
 ACCESSION U33831.1 GI:2754700
 VERSION U33831.1
 KEYWORDS
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 590)
 AUTHORS Blasco, M.A., Funk, W., Villeponteau, B. and Greider, C.W.
 TITLE Functional characterization and developmental regulation of mouse
 telomerase RNA
 JOURNAL Science 269 (5228), 1267-1270 (1995)
 MEDLINE 95381063
 PUBMED 7544492
 REFERENCE 2 (bases 1 to 114)
 AUTHORS Hinkley, C.S., Blasco, M.A., Feng, J., Villeponteau, B., Greider, C.W.
 and Herr, W.
 TITLE The mouse telomerase RNA 5' end lies just upstream of the telomerase
 template sequence
 JOURNAL Nucleic Acids Res. (1998) In press
 REFERENCE 3 (bases 1 to 590)
 AUTHORS Blasco, M.A., Funk, W., Villeponteau, B. and Greider, C.W.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-1995) Carol W. Greider, Cold Spring Harbor
 Laboratory, PO Box 100, 1 Bungtown Road, Cold Spring Harbor, NY
 11724, USA
 REFERENCE 4 (bases 1 to 590)
 AUTHORS Blasco, M.A., Funk, W., Villeponteau, B. and Greider, C.W.
 TITLE Direct Submission
 JOURNAL Submitted (03-DEC-1997) Carol W. Greider, Cold Spring Harbor
 Laboratory, PO Box 100, 1 Bungtown Road, Cold Spring Harbor, NY
 11724, USA
 REFERENCE 5 (bases 1 to 590)
 AUTHORS Blasco, M.A., Funk, W., Villeponteau, B. and Greider, C.W.
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-1998) Carol W. Greider, Cold Spring Harbor
 Laboratory, PO Box 100, 1 Bungtown Road, Cold Spring Harbor, NY
 11724, USA
 REMARK Sequence update by submitter
 COMMENT On Jan 7, 1998 this sequence version replaced gi:2660646.
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 /note="Initially cloned from D3 embryonic stem cell
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 conservation with the human homolog the 3' end is near
 position 484 in this sequence"
 30
 /note="transcription start site"
 92..99
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 synthesis of the telomere sequence TTAGGG"

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 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 GGAAGAGGAGGACATTTCCGCAAGTGTGGGCTCGACCAATCAGCGCGCCATGAGGATA 520
 DB 1 GGAAGAGGAGGACATTTCCGCAAGTGTGGGCTCGACCAATCAGCGCGCCATGAGGATA 60
 QY 521 TTAAAGTGTGAGGCGGCTAGGCGCTCGGACCTTAACCTGATTTTCTAGTGTGAGGTT 580
 DB 61 TTAAAGTGTGAGGCGGCTAGGCGCTCGGACCTTAACCTGATTTTCTAGTGTGAGGTT 120
 QY 581 CTGTCCTTTGTCTCCGCGGCTGTTTCTCGCTGACTTCAGCG 628

Db 121 CCGGCTTTTGTTCCTCCGCCCGCTGTTTCTTCGCTGACTTCAGCGG 168

RESULT 13
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DEFINITION AC139643 220807 bp DNA linear HTG 27-MAR-2003
uncloned pieces.
AC139643
AC139643.1 GI:28273299
HTG: HTGS PHASE1; HTGS DRAFT
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 220807)
Muzny, D., Maric, M., Metzker, M., Lee, A., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Aml, A., Angiano, D.,
Anyalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Burch, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cre, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denison, S., Derano, C., Ding, Y., Dinh, H., Divya, K.,
Drager, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebrgeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M.,
Hollins, B., Howells, S., Hu, J., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, J., Kovar, C.,
Kows, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshaw, L., Louleghed, H., Lozano, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, R., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,
Miner, G., Mijic, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Morris, S., Mundana, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okunolu, G.,
Olanunso, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A.,
Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E.,
Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,
Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojars, A.,
Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S.,
Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
Sisson, I., Sitter, C.D., Smajda, D., Sneed, A., Sodergren, E.,
Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A.,
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingley, A., Trejos, Z., Usmant, K., Valae, R., Vera, V., Villaseana, D.,
Walton, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, X.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R.,
Hol, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 220807)
Unpublished
Direct Submission
Worley, K.C.
Submitted (08-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 220807)
Worley, K.C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KDRD
Center clone name: CH230-208P8
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 184542 bases at least Q40
Consensus quality: 191076 bases at least Q30
Consensus quality: 195268 bases at least Q20
Estimated insert size: 194058; sum-of-coverage estimation
Quality coverage: 3x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1573: gap of unknown length
1673: contig of 1357 bp in length
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3030: gap of unknown length
3129: gap of unknown length
3130: contig of 1725 bp in length
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4855: gap of unknown length
4954: gap of unknown length
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6309: gap of unknown length
6210: gap of unknown length
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7826: contig of 1517 bp in length
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7927: contig of 1123 bp in length
9049: gap of unknown length
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9150: contig of 1269 bp in length
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10519: gap of unknown length
10519: contig of 1651 bp in length
12169: gap of unknown length
12170: gap of unknown length
12270: contig of 1495 bp in length
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13865: contig of 157 bp in length
13865: gap of unknown length
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15321: gap of unknown length
16370: contig of 1049 bp in length
15322: gap of unknown length
16470: gap of unknown length
16471: gap of unknown length
16471: contig of 1588 bp in length
18058: gap of unknown length
18059: gap of unknown length
18158: gap of unknown length
20066: contig of 1848 bp in length
20067: gap of unknown length
20107: gap of unknown length
21894: contig of 1788 bp in length
21994: gap of unknown length
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24019: contig of 2025 bp in length
24020: gap of unknown length
24119: gap of unknown length
24120: contig of 2699 bp in length
26818: gap of unknown length
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30012: contig of 3094 bp in length
30112: gap of unknown length
30113: gap of unknown length
30113: contig of 2633 bp in length
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32746: gap of unknown length
32845: contig of 3901 bp in length
32846: gap of unknown length
36746: gap of unknown length
36747: gap of unknown length

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					Gaps	5;
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[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (pages 1 to 481)
Chen, J.-L., Blasco, M.A. and Greider, C.W.
Direct Substitution
Submitted (06-JUN-2000) Molecular Biology and Genetics, Johns ...

FEATURES	Location/Qualifiers
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Matches 115; Conservative	0;	Mismatches 23;	Indels 2;	Gaps 1

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Db	93	CGTTCAACCCATTTGTT--ATAGCTGAGGATTCGTCTTTTGTCTCCGCGCCGCTTT	150
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RESULT 15				
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LOCUS				
DEFINITION	397 bp	DNA	linear	ROD 20-MAR-2007
	Mus musculus caetaneus telomerase RNA, genomic sequence.			

ACCESSION AY058900
 VERSION AY058900.1 GI:16751329
 KEYWORDS
 SOURCE Mus musculus castaneus (southeastern Asian house mouse)
 ORGANISM Mus musculus castaneus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 397)
 Hatcher, K.S., Hemann, M.T., Opperman, K.K., Strong, M.A.,
 Greider, C.W. and Hodes, R.J.
 Haploinsufficiency of mTR results in defects in telomere elongation
 Proc. Natl. Acad. Sci. U.S.A. 99 (6), 3591-3596 (2002)
 11904421
 REFERENCE 2 (bases 1 to 397)
 Hemann, M.T. and Greider, C.W.
 Direct Submision
 Submitted (09-OCT-2001) Molecular Biology and Genetics, Johns
 Hopkins University School of Medicine, 725 N. Wolfe St., Hunterian
 617, Baltimore, MD 21205, USA
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 DB 1 ACCTAACCTGATTTCATTAGCTGTGGTCTGTGCTTTGTTCTCCGCCGCTGTTT 60
 QY 610 TCTCGCTGACTTCCACGG 628
 DB 61 TCTCGCTGACTTCCACGG 79

Search completed: April 26, 2005, 18:27:29
 Job time : 3012.16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using BW model

Run on: April 26, 2005, 18:27:34 ; Search time 646.625 Seconds

(without alignments)
8140.109 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867
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Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications NA.*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	848.6	97.9	2426	9	US-09-057-351-3
2	848.6	97.9	2426	14	US-10-206-447-2
3	848.6	97.9	2426	16	US-10-353-935-3
4	333	38.4	981	10	US-09-895-606-5
5	163	18.8	545	17	US-10-388-360-384
6	163	18.8	545	18	US-10-831-266-2
7	163	18.8	545	19	US-10-831-267-2
8	110.8	12.6	340449	12	US-09-903-582-3
9	109.2	12.6	133893	13	US-10-161-510-1
10	108.8	12.5	201	18	US-10-741-601-25989
11	108.8	12.5	27240	18	US-10-741-601-5777

C 12	108.6	12.5	76698	19	US-10-936-273-30	Sequence 30, Appl
C 13	107.6	12.4	52899	17	US-10-085-117-148	Sequence 148, App
C 14	106.2	12.2	22275	17	US-10-104-047-453	Sequence 453, App
C 15	106.2	12.2	313267	18	US-10-322-281-48	Sequence 48, Appl
C 16	106	12.2	1286	13	US-10-027-632-202645	Sequence 202645,
C 17	106	12.2	1286	17	US-10-027-632-202645	Sequence 202645,
C 18	106	12.2	138837	18	US-10-322-281-146	Sequence 146, App
C 19	104.8	12.1	2133	17	US-10-108-260A-468	Sequence 468, App
C 20	104.8	12.1	26528	17	US-10-374-979-6	Sequence 6, Appl
C 21	104.8	12.1	26528	17	US-10-182-936A-6	Sequence 6, Appl
C 22	104.8	12.1	26528	18	US-10-731-739-6	Sequence 6, Appl
C 23	104.8	12.1	26528	18	US-10-477-238A-6	Sequence 6, Appl
C 24	104.8	12.1	26528	18	US-10-680-287A-6	Sequence 6, Appl
C 25	104.8	12.1	26528	19	US-10-477-173-6	Sequence 6, Appl
C 26	104.8	12.1	156843	13	US-10-087-192-1408	Sequence 1408, A
C 27	104.4	12.0	46878	19	US-10-741-600-17664	Sequence 17664, A
C 28	104.4	12.0	54945	10	US-09-967-669-10	Sequence 10, Appl
C 29	104.4	12.0	76410	13	US-10-087-192-70	Sequence 70, Appl
C 30	104.4	12.0	115935	18	US-10-775-169-241	Sequence 241, App
C 31	104.4	12.0	168749	17	US-10-085-117-250	Sequence 250, App
C 32	104.4	12.0	220895	18	US-10-775-169-88	Sequence 88, Appl
C 33	104.4	12.0	301692	17	US-10-428-487-11	Sequence 11, Appl
C 34	104.4	12.0	310268	18	US-10-367-094-195	Sequence 195, App
C 35	104.4	12.0	493399	18	US-10-719-993-6787	Sequence 6787, Ap
C 36	104.4	12.0	32134	10	US-09-764-891-6303	Sequence 6303, Ap
C 37	104	12.0	32134	15	US-10-205-428-608	Sequence 608, App
C 38	104	12.0	32191	10	US-09-764-891-6304	Sequence 6304, Ap
C 39	104	12.0	32191	15	US-10-205-428-609	Sequence 609, App
C 40	104	12.0	55114	13	US-10-087-192-1606	Sequence 1606, Ap
C 41	104	12.0	86361	18	US-10-741-601-17803	Sequence 17803, A
C 42	104	12.0	86361	19	US-10-741-600-17772	Sequence 554, App
C 43	103.6	11.9	43103	18	US-10-322-281-554	Sequence 17772, A
C 44	103.6	11.9	43103	19	US-10-741-600-17772	Sequence 17772, A
C 45	103.2	11.9	653122	13	US-10-087-192-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-09-057-351-3
; Sequence 3, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Unli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-UTL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-057-351-3
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Query Match          97.9%; Score 848.6; DB 9; Length 2426;
Best Local Similarity 99.4%; Pred. No. 2.5e-253;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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QY 61 AGCCGAGATCAGCCGCTGACCTCCATCCAGCCTGGGCGGAAAGACAAAGACTCCGCTCA 120
DB 721 AGCCGAGATCAGCCGCTGACCTCCATCCAGCCTGGGCGGAAAGACAAAGACTCCGCTCA 780
QY 121 AAAAAAAAAATCGTTACATTTATGTTGATTAATCTCCCTCTTTTACCTCATCAAGACA 180
DB 781 AAAAAAAAAATCGTTACATTTATGTTGATTAATCTCCCTCTTTTACCTCATCAAGACA 840
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DB 841 CAGCACTACTTTAAGCAAAAGTCAATGATTGAAAGCCCTTCTTCTTAATAAAGGAG 900
QY 241 ATTCACTCTTGAATTAATATATGATGATTAATCACTTAATTAAGCAATCCCTGCTCA 300
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QY 361 CCACTGAGCCGAGACAAAGATTCTGCTGATGTCAGTCTGCTCGGAAATCTATTTTCA 420
DB 1021 CCACTGAGCCGAGACAAAGATTCTGCTGATGTCAGTCTGCTCGGAAATCTATTTTCA 1080
QY 421 AGTTCTCCAAAAAATGATGATCAAAATAGGAATTAATGTTCTGTCTTAGGCCCTA 480
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QY 601 TAAAGACGCAAGCCCTTCCCGGACGTGCGAAGGGCAAGTCTTCTCATGCGGAA 660
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DB 1321 ATGGAACCTTAATTTCCGTTCCCGCAACAGCCCGCCGAGAGATGACTCTCAGAG 1380
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QY 841 TGTCTAACCTTAATCTGAAGAGGGCCCTA 867
DB 1501 TGTCTAACCTTAATCTGAAGAGGGCCCTA 1527
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RESULT 2

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US-10-206-447-2
; Sequence 2, Application US/10206447
; Publication No. US20030099616A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving, John
; APPLICANT: Karpf, David
; APPLICANT: Schiff, Michael
; TITLE OF INVENTION: DNA SPECIFICITY TUMOR KILLING VECTORS DRIVEN BY THE TELOMERASE P
; FILE REFERENCE: 085/002
; CURRENT APPLICATION NUMBER: US/10/206,447
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,029
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-447-2
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Query Match          97.9%; Score 848.6; DB 14; Length 2426;
Best Local Similarity 99.4%; Pred. No. 2.5e-253;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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QY 1 AGCTACTCAGAGGCTTGAGACACGAGAAATCGTTGAACCCGGAGGACAGAGTTGCAGTG 60
DB 662 AGCTACTCAGAGGCTTGAGACACGAGAAATCGTTGAACCCGGAGGACAGAGTTGCAGTG 720
QY 61 AGCCGAGATCAGCCGCTGACCTCCATCCAGCCTGGGCGGAAAGACAAAGCTCCGCTCA 120
DB 721 AGCCGAGATCAGCCGCTGACCTCCATCCAGCCTGGGCGGAAAGACAAAGCTCCGCTCA 780
QY 121 AAAAAAAAAATCGTTACATTTATGTTGATTAATCTCCCTCTTTTACCTCATCAAGACA 180
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QY 181 CAGCACTACTTTAAGCAAAAGTCAATGATTGAAAGCCCTTCTTCTTAATAAAGGAG 240
DB 841 CAGCACTACTTTAAGCAAAAGTCAATGATTGAAAGCCCTTCTTCTTAATAAAGGAG 900
QY 241 ATTCACTCTTGAATTAATATATGATGATTAATCACTTAATTAAGCAATCCCTGCTCA 300
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DB 1021 CCACTGAGCCGAGACAAAGATTCTGCTGATGTCAGTCTGCTCGGAAATCTATTTTCA 1080
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DB 1081 AGTTCTCCAAAAAATGATGATCAAAATAGGAATTAATGTTCTGTCTTAGGCCCTA 1140
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; Publication No. US20030207404A1
; GENERAL INFORMATION:
; APPLICANT: Villeneuve, Bryant
;           Peng, Junli
;           Andrews, William H.
;           Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
;                   Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,606
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/710,249
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 267..715
; OTHER INFORMATION: /product= "hTR"
; /note= "hTR transcript serves as
;         template in the telomerase
;         ribonucleoprotein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-895-606-5

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Best Local Similarity 99.7%; Pred. No. 9,99-93;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 534 CTGCAGAGATGAGAAAAAGCCCTGTACTCAATCTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAGAAAAAGCCCTGTACTCAATCTTACCTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGACGCAAGCCTTCTCCGAGCGTGGAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTCTCCGAGCGTGGAGGCAACGTCCTTCATG 120
QY 654 GCCGGAATGGAATTTATTTCCGTTCCCAACGAGCCGCCCGGAGAGAGTCACTC 713
DB 121 GCCGGAATGGAATTTATTTCCGTTCCCAACGAGCCGCCCGGAGAGAGTCACTC 180
QY 714 TCACGAGAGCCCGAGAGTCACTTGGCCATCCGTCGCGTGGCGGCGCTCCCTTAT 773
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QY 774 AAGCCGACTCGCCCGGACGCAACCGGATTGGAGGGGTGGAGGGGTGGTGC 833
DB 241 AAGCCGACTCGCCCGGACGCAACCGGATTGGAGGGGTGGAGGGGTGGTGC 300
QY 834 CATTTTTGTCTAACCTTAAGAGAGGCGCTA 867
DB 301 CATTTTTGTCTAACCTTAAGAGAGGCGCTA 334

RESULT 5
US-10-388-360-384
; Sequence 384, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffe B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-384

Query Match      18.8%; Score 163; DB 17; Length 545;
Best Local Similarity 100.0%; Pred. No. 7,66-40;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GAGTACTCTACGAGAGCCCGGAGAGTCACTTGGCCATTCGTGCGTGGCGGCGG 60
QY 765 TCCCTTTAAGCCGACTCGCCCGGACCGGACCGGGTTGCGAGGGTGGCTTGGAGG 824
DB 61 TCCCTTTAAGCCGACTCGCCCGGACCGGACCGGGTTGCGAGGGTGGCTTGGAGG 120
QY 825 GGTGTGGCCATTTTGTCTAACCTTAAGAGAGGCGCTA 867
DB 121 GGTGTGGCCATTTTGTCTAACCTTAAGAGAGGCGCTA 163

RESULT 6
US-10-831-266-2
; Sequence 2, Application US/10831266
; Publication No. US20050003404A1
; GENERAL INFORMATION:
; APPLICANT: Rowley, Peter T.
; TITLE OF INVENTION: TELOMERASE INTERFERENCE
; FILE REFERENCE: A-71506-1/RFT/THR
; CURRENT APPLICATION NUMBER: US/10/831,266
; PRIOR FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: PCT/US 02/33065
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/345,326
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/359,196
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/383,195
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 17

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SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-831-267-2

Query Match 18.8%; Score 163; DB 18; Length 545;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 705 GAGTGAAGTCTCAAGAGAGCCGCGAGAGTCAAGCTTGGCCCAATCCGTCGTCGCGCGCCG 764
DB 1 GAGTGAAGTCTCAAGAGAGCCGCGAGAGTCAAGCTTGGCCCAATCCGTCGTCGCGCGCCG 60
QY 765 TCCCTTTATTAAGCCGAGCTGCGCCGCGAGCGCACCGGGTTGCGAGGGGTGGGCTTGGAGG 824
DB 61 TCCCTTTATTAAGCCGAGCTGCGCCGCGAGCGCACCGGGTTGCGAGGGGTGGGCTTGGAGG 120
QY 825 GGTGGTGGCCATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 121 GGTGGTGGCCATTTTGTCTAACCTTAAGTGAAGGGCGTA 163

RESULT 7
US-10-831-267-2
; Sequence 2, Application US/10831267
; Publication No. US2005009177A1
; GENERAL INFORMATION:
; APPLICANT: Rowley, Peter T.
; TITLE OF INVENTION: TELOMERASE INTERFERENCE
; FILE REFERENCE: A-71506-2/RFT/THR
; CURRENT APPLICATION NUMBER: US/10/831,267
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: PCT/US 02/33146
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/345,326
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/359,196
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/383,195
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-831-267-2

Query Match 18.8%; Score 163; DB 19; Length 545;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 705 GAGTGAAGTCTCAAGAGAGCCGCGAGAGTCAAGCTTGGCCCAATCCGTCGTCGCGCGCCG 764
DB 1 GAGTGAAGTCTCAAGAGAGCCGCGAGAGTCAAGCTTGGCCCAATCCGTCGTCGCGCGCCG 60
QY 765 TCCCTTTATTAAGCCGAGCTGCGCCGCGAGCGCACCGGGTTGCGAGGGGTGGGCTTGGAGG 824
DB 61 TCCCTTTATTAAGCCGAGCTGCGCCGCGAGCGCACCGGGTTGCGAGGGGTGGGCTTGGAGG 120
QY 825 GGTGGTGGCCATTTTGTCTAACCTTAAGTGAAGGGCGTA 867
DB 121 GGTGGTGGCCATTTTGTCTAACCTTAAGTGAAGGGCGTA 163

RESULT 8
US-09-903-582-3
; Sequence 3, Application US/09903582
; Publication No. US20050075283A1
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al.

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001274
; CURRENT APPLICATION NUMBER: US/09/903,582
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatSeQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 340449
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(340449)
; OTHER INFORMATION: n = A,T,C or G
US-09-903-582-3

Query Match 12.8%; Score 110.8; DB 12; Length 340449;
Best Local Similarity 90.8%; Pred. No. 4.8e-22;
Matches 118; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACACGAAATCGCTTGAACCCGGGAGGACAGAGTTGCAGTG 60
DB 249884 AGCTACTCAGAGGCTGAGAGCATGAAATCGCTTGAATCCGGGAGGACAGAGTTGCAGTG 249943
QY 61 AGCCGAGATCAGCCCACTGACTGATCCATCCAGCTTGGGCGAAGACAACTCCGCTCA 120
DB 249944 AACTGATGCGGCGCACTGCACTCCATCCAGCTTGGGCGAAGAGTGAAGTCCGCTCA 250003
QY 121 AAAAAAAAAA 130
DB 250004 AAAAAAAAAA 250013

RESULT 9
US-10-161-510-1/c
; Sequence 1, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PIBS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-074C
; CURRENT APPLICATION NUMBER: US/10/161,510
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 133893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-510-1

Query Match 12.6%; Score 109.2; DB 13; Length 133893;
Best Local Similarity 90.0%; Pred. No. 9.1e-22;
Matches 117; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACACGAAATCGCTTGAACCCGGGAGGACAGAGTTGCAGTG 60
DB 63711 AGCTACTCAGAGGCTGAGAGCGAGAAATGCGTGAACCCGGGAGGAGGCTTGCAGTG 63652
QY 61 AGCCGAGATCAGCCCACTGACTGATCCATCCAGCTTGGGCGAAGACAAAGTCCGCTCA 120
DB 63651 AGCCGAGATCAGCCCACTGACTGATCCATCCAGCTTGGGCGAGAGTCCGCTCA 63592
QY 121 AAAAAAAAAA 130

Db 63591 AAAAAAAAAA 63582

RESULT 10

US-10-741-601-25989/c
 ; Sequence 25989, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001500
 ; CURRENT APPLICATION NUMBER: US/10/741,601
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 25989
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-601-25989

Query Match 12.5%; Score 108.8; DB 18; Length 201;
 Best Local Similarity 89.2%; Pred. No. 3,5e-23;
 Matches 116; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACAGGAATCGCTTGAACCGGGAGGCGAGGCTTGACATG 60
 |||||
 DB 132 AGCTACTCGGAGGCTGAGACAGGAATGSGTGAACCGGGAGGCGAGGCTTGACATG 73
 |||||
 QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGCGGAAAGAGCAAGACTCCGTTCA 120
 |||||
 DB 72 AGCCGAGATCAGCCCACTAGACTCCATCCAGCATGGGTGACAGAGCGAGACTCCGTTCA 13
 |||||
 QY 121 AAAAAAAAAA 130
 |||||
 DB 12 AAAAAAAAAA 3

RESULT 11

US-10-741-601-5777/c
 ; Sequence 5777, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001500
 ; CURRENT APPLICATION NUMBER: US/10/741,601
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5777
 ; LENGTH: 27240
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-601-5777

Query Match 12.5%; Score 108.8; DB 18; Length 27240;
 Best Local Similarity 89.2%; Pred. No. 5,1e-22;
 Matches 116; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACAGGAATCGCTTGAACCGGGAGGCGAGGCTTGACATG 60
 |||||
 DB 11618 AGCTACTCGGAGGCTGAGACAGGAATGSGTGAACCGGGAGGCGAGGCTTGACATG 11559
 |||||
 QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGCGGAAAGAGCAAGACTCCGTTCA 120
 |||||
 DB 11588 AGCCGAGATCAGCCCACTAGACTCCATCCAGCATGGGTGACAGAGCGAGACTCCGTTCA 11499
 |||||
 QY 121 AAAAAAAAAA 130
 |||||
 DB 11498 AAAAAAAAAA 11489

RESULT 12

US-10-936-273-30/c
 ; Sequence 30, Application US/10936273
 ; Publication No. US20050074801A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Montia, Brett P.
 ; APPLICANT: Butler, Madeline M.
 ; APPLICANT: McKay, Robert
 ; APPLICANT: Baker, Brenda F.
 ; TITLE OF INVENTION: CHIMERIC OLIGOMERIC COMPOUNDS COMPRISING ALTERNATING REGIONS OF N
 ; TITLE OF INVENTION: AND SOUTHERN CONFORMATIONAL GEOMETRY
 ; FILE REFERENCE: ISIS0104-100 (CORE002605)
 ; CURRENT APPLICATION NUMBER: US/10/936,273
 ; CURRENT FILING DATE: 2004-09-08
 ; NUMBER OF SEQ ID NOS: 221
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 76698
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 15311-15410
 ; OTHER INFORMATION: n = A,T,C or G
 ; NAME/KEY: misc.feature
 ; LOCATION: 15414
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-936-273-30

Query Match 12.5%; Score 108.6; DB 19; Length 76698;
 Best Local Similarity 81.3%; Pred. No. 1e-21;
 Matches 126; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACAGGAATCGCTTGAACCGGGAGGCGAGGCTTGACATG 60
 |||||
 DB 15588 AGCTACTCAGAGGCTGAGACAGGAATGCGATGAACCGGGAGGCGAGGCTTGACATG 15529
 |||||
 QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGCGGAAAGAGCAAGACTCCGTTCA 120
 |||||
 DB 15528 AGCCGAGATCAGCCCACTAGACTCCATCCAGCCTGGCGGAGAGCGAGACTCGTTCA 15469
 |||||
 QY 121 AAAAAAAAAATCGTACATTTATGATGATTAAGT 155
 |||||
 DB 15468 AAAAAAAAAAAAAAAAAAGGCGAGGCTTAAGT 15434

RESULT 13

US-10-085-117-148/c
 ; Sequence 148, Application US/10085117
 ; Publication No. US2003023234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: 529452000121
 ; CURRENT APPLICATION NUMBER: US/10/085,117
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 09/799,586
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 148
 ; LENGTH: 52899
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (1)...(52899)
 ; OTHER INFORMATION: n = any nucleotide
 US-10-085-117-148

Query Match 12.4%; Score 107.6; DB 17; Length 52899;
 Best Local Similarity 89.2%; Pred. No. 1.7e-21;
 Matches 116; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACACGAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
 |||||
 DB 49315 AGCTACTCGGAGGCTGAGGCGAGAGAAATGGCTTGAACCCGGAGGCGAGGCTTGCAGTG 49256
 |||||
 QY 61 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAAGACTCCGTTCTCA 120
 |||||
 DB 49255 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAAGACTCCGTTCTCA 49196
 |||||
 QY 121 AAAAAAAAAA 130
 |||||
 DB 49195 AAAAAAAAAA 49186

RESULT 14
 US-10-104-047-453/c

; Sequence 453, Application US/10104047
 ; Publication No. US20030236392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 453
 ; LENGTH: 2275
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-104-047-453

Query Match 12.2%; Score 106.2; DB 17; Length 2275;
 Best Local Similarity 83.9%; Pred. No. 8.6e-22;
 Matches 120; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACACGAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
 |||||
 DB 1535 AGCTACTCGGAGGCTGAGGCGAGAGAAATGGCTTGAACCCGGAGGCGAGGCTTGCAGTG 1476
 |||||
 QY 61 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAAGACTCCGTTCTCA 120
 |||||
 DB 1475 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAAGACTCCGTTCTCA 1416
 |||||
 QY 121 AAAAAAAAAATCGTTACAATTAA 143
 |||||
 DB 1415 AAAAAAAAAATCGTTACAATTAA 1393

RESULT 15

US-10-322-281-48/c
 ; Sequence 48, Application US/10322281
 ; Publication No. US20040126762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: David W. Morris
 ; APPLICANT: Marc S. Malandro
 ; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
 ; FILE REFERENCE: 529452001000
 ; CURRENT APPLICATION NUMBER: US/10/322,281
 ; CURRENT FILING DATE: 2002-12-17
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 313287
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

; NAME/KEY: misc feature
 ; LOCATION: (1)-(313287)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-322-281-48

Query Match 12.2%; Score 106.2; DB 18; Length 313287;
 Best Local Similarity 83.9%; Pred. No. 1.3e-20;
 Matches 120; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACACGAGAAATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60
 |||||
 DB 133419 AGCTACTCAGAGGCTGAGGCGAGAGAAATCGCTTGAACCCGGAGGCGAGGCTTGCAGTG 133360
 |||||
 QY 61 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAAGACTCCGTTCTCA 120
 |||||
 DB 133359 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAAGACTCCGTTCTCA 133300
 |||||
 QY 121 AAAAAAAAAATCGTTACAATTAA 143
 |||||
 DB 133299 AAAAAAAAAAAAAAAAAAGTTAA 133277

Search completed: April 26, 2005, 22:56:08
 Job time : 651.625 secs

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:02:08 ; Search time 187.318 Seconds
(without alignments)
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Title: US-09-601-267-36

Perfect score: 867
Sequence: 1 agctactcagagcgctcga.....ccctactcgaagcgcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	848.6	97.9	2420	1 US-08-330-123A-3	Sequence 3, Appl1
2	848.6	97.9	2420	3 US-09-580-517-3	Sequence 3, Appl1
3	848.6	97.9	2426	1 US-08-482-115B-3	Sequence 3, Appl1
4	848.6	97.9	2426	2 US-08-660-678A-3	Sequence 3, Appl1
5	848.6	97.9	2426	2 US-08-472-802C-4	Sequence 4, Appl1
6	848.6	97.9	2426	2 US-08-714-482-1	Sequence 1, Appl1
7	848.6	97.9	2426	3 US-08-998-443-3	Sequence 3, Appl1
8	848.6	97.9	2426	3 US-09-060-523-3	Sequence 3, Appl1
9	848.6	97.9	2426	4 US-09-057-351-3	Sequence 3, Appl1
10	834.6	96.3	2425	2 US-08-485-778-1	Sequence 1, Appl1
11	834.6	96.3	2425	3 US-08-520-550A-1	Sequence 1, Appl1
12	334	38.5	981	2 US-08-114-482-2	Sequence 2, Appl1
13	333	38.4	981	2 US-08-710-249-5	Sequence 5, Appl1
14	333	38.4	981	3 US-09-220-157A-5	Sequence 1, Appl1
15	332.4	38.3	981	2 US-08-770-565-1	Sequence 1, Appl1
16	332.4	38.3	981	2 US-08-833-377-1	Sequence 2, Appl1
17	332.4	38.3	981	3 US-08-838-545-22	Sequence 22, Appl1
18	332.4	38.3	981	3 US-09-349-532-22	Sequence 22, Appl1
19	110.8	12.8	601	4 US-09-949-016-73377	Sequence 73377, A
20	110.8	12.8	601	4 US-09-949-016-12610	Sequence 12610, A
21	110.8	12.8	601	4 US-09-949-016-13880	Sequence 13880, A
22	109.4	12.6	601	4 US-09-949-016-87488	Sequence 87488, A
23	109.4	12.6	601	4 US-09-949-016-12505	Sequence 12505, A
24	109.4	12.6	601	4 US-09-949-016-14207	Sequence 14207, A
25	109.4	12.6	601	4 US-09-949-016-87489	Sequence 87489, A
26	108	12.5	601	4 US-09-949-016-87487	Sequence 87487, A
27	107.6	12.4	601	4 US-09-949-016-204713	Sequence 204713, A

28	107.6	12.4	50530	4 US-09-949-016-12163	Sequence 12163, A
29	107.6	12.4	50536	4 US-09-949-016-17526	Sequence 17526, A
30	107	12.3	134140	4 US-09-949-016-12572	Sequence 12572, A
31	107	12.3	134281	4 US-09-949-016-12824	Sequence 12824, A
32	107	12.3	134282	4 US-09-949-016-15813	Sequence 15813, A
33	107	12.3	134282	4 US-09-949-016-15814	Sequence 15814, A
34	107	12.3	134282	4 US-09-949-016-15815	Sequence 15815, A
35	106	12.2	601	4 US-09-949-016-143018	Sequence 143018, A
36	106	12.2	601	4 US-09-949-016-143019	Sequence 143019, A
37	106	12.2	19601	4 US-09-949-016-15629	Sequence 15629, A
38	106	12.2	265038	4 US-09-949-016-15779	Sequence 15779, A
39	105	12.1	601	4 US-09-949-016-55951	Sequence 55951, A
40	105	12.1	601	4 US-09-949-016-55952	Sequence 55952, A
41	105	12.1	601	4 US-09-949-016-55953	Sequence 55953, A
42	105	12.1	25111	4 US-09-949-016-12435	Sequence 12435, A
43	105	12.1	25111	4 US-09-949-016-13944	Sequence 13944, A
44	105	12.1	53442	4 US-09-949-016-11921	Sequence 11921, A
45	105	12.1	53453	4 US-09-949-016-13370	Sequence 13370, A

ALIGNMENTS

RESULT 1
US-08-330-123A-3
; Sequence 3, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLOPONTAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2420 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; STRANDEDNESS: single
; MOLECULE TYPE: DNA (genomic)
; US-08-330-123A-3
Query Match 97.9%; Score 848.6; DB 1; Length 2420;
Best Local Similarity 99.4%; Pred. No. 1.6e-274;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGAGAGGTTGCACTG 60
DB 662 AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGAGAGGTTGCACTG 720
QY 61 AGCCGAGATCAGCCCACTAGACTCATCCAGCTGAGGAGAAAGCAAGACTCCGCTCA 120
DB 721 AGCCGAGATCAGCCCACTAGACTCATCCAGCTGAGGAGAAAGCAAGACTCCGCTCA 780
QY 121 AAAAAAAAAATCGTTACATTTATGTGTGATTAATCTCCCTCTTTTAACTCATCAAGCA 180
DB 781 AAAAAAAAAATCGTTACATTTATGTGTGATTAATCTCCCTCTTTTAACTCATCAAGCA 840
QY 181 CAGCACTACTTAAAGCAAGTCAATGATTAAGAAAGGCTTCTTCTTAATAAAGGAG 240
DB 841 CAGCACTACTTAAAGCAAGTCAATGATTAAGAAAGGCTTCTTCTTAATAAAGGAG 900
QY 241 ATTCACTCTTAAAGTATTAATGATTAATGATTAATCACTTGAATTAAGCACTCTGCTCA 300
DB 901 ATTCACTCTTAAAGTATTAATGATTAATGATTAATCACTTGAATTAAGCACTCTGCTCA 960
QY 301 AGGAGAGGCTGAGAGAGGCTTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 961 AGGAGAGGCTGAGAGAGGCTTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 361 CCACTGAGCCGAGACAAAGATTCGTGTGATGATGATGATGATGATGATGATGATGAT 420
DB 1021 CCACTGAGCCGAGACAAAGATTCGTGTGATGATGATGATGATGATGATGATGATGAT 1080
QY 421 AGTTCTCCAAAAATGATGATCAAAACTAGAAATTAAGTTTCTGTGTCTTAAGGCTCA 480
DB 1081 AGTTCTCCAAAAATGATGATCAAAACTAGAAATTAAGTTTCTGTGTCTTAAGGCTCA 1140
QY 481 AAATCTCTCGTGAATTCATTTTAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
DB 1141 AAATCTCTCGTGAATTCATTTTAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1200
QY 541 GGATAGAAAAAGAGGCTCTGATGATCACTCAATTAAGTTTCACTTAAAGAGTGAAG 600
DB 1201 GGATAGAAAAAGAGGCTCTGATGATCACTCAATTAAGTTTCACTTAAAGAGTGAAG 1260
QY 601 TAAAGAGCAAAAGCTTTTCCCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 1261 TAAAGAGCAAAAGCTTTTCCCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 661 ATGGAATCTTAAATTTCCCGTCCCGCAACAGCCCGCCGAGAGAGAGAGAGAGAGAG 720
DB 1321 ATGGAATCTTAAATTTCCCGTCCCGCAACAGCCCGCCGAGAGAGAGAGAGAGAGAG 1380
QY 721 AGCCGAGAGTCAAGCTTGGCCCAATCGTGGGCTGGGCGGCTCTCTTAAAGCCGA 780
DB 1381 AGCCGAGAGTCAAGCTTGGCCCAATCGTGGGCTGGGCGGCTCTCTTAAAGCCGA 1440
QY 781 CTGCGCCGAG 840
DB 1441 CTGCGCCGAG 1500
QY 841 TGTCTAACCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
DB 1501 TGTCTAACCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527

RESULT 2

US-09-580-517-3

Sequence 3, Application us/09580517

Patent No. 6320039

GENERAL INFORMATION:

APPLICANT: VILLEPONTBAU, Bryant

FENG, Junli

FUNK, Walter

ANDREWS, William H.

TITLE OF INVENTION: HUMAN TELOMERASE

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-580-517-3

Query Match 97.9%; Score 848.6; DB 3; Length 2420;
Best Local Similarity 99.4%; Pred. No. 1.6e-274;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGAGAGGTTGCACTG 60
DB 662 AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGAGAGGTTGCACTG 720
QY 61 AGCCGAGATCAGCCCACTAGACTCATCCAGCTGAGGAGAAAGCAAGACTCCGCTCA 120
DB 721 AGCCGAGATCAGCCCACTAGACTCATCCAGCTGAGGAGAAAGCAAGACTCCGCTCA 780
QY 121 AAAAAAAAAATCGTTACATTTATGTGTGATTAATCTCCCTCTTTTAACTCATCAAGCA 180
DB 781 AAAAAAAAAATCGTTACATTTATGTGTGATTAATCTCCCTCTTTTAACTCATCAAGCA 840
QY 181 CAGCACTACTTAAAGCAAGTCAATGATTAAGAAAGGCTTCTTCTTAATAAAGGAG 240
DB 841 CAGCACTACTTAAAGCAAGTCAATGATTAAGAAAGGCTTCTTCTTAATAAAGGAG 900
QY 241 ATTCACTCTTAAAGTATTAATGATTAATGATTAATCACTTGAATTAAGCACTCTGCTCA 300
DB 901 ATTCACTCTTAAAGTATTAATGATTAATGATTAATCACTTGAATTAAGCACTCTGCTCA 960
QY 301 AGGAGAGGCTGAGAGAGGCTTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 961 AGGAGAGGCTGAGAGAGGCTTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 361 CCACTGAGCCGAGACAAAGATTCGTGTGATGATGATGATGATGATGATGATGATGAT 420
DB 1021 CCACTGAGCCGAGACAAAGATTCGTGTGATGATGATGATGATGATGATGATGATGAT 1080
QY 421 AGTTCTCCAAAAATGATGATCAAAACTAGAAATTAAGTTTCTGTGTCTTAAGGCTCA 480
DB 1081 AGTTCTCCAAAAATGATGATCAAAACTAGAAATTAAGTTTCTGTGTCTTAAGGCTCA 1140
QY 481 AAATCTCTCGTGAATTCATTTTAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540

Db 1141 AATCTTCCTGTAATTCATTTTAAAGTAGTCAGATGAAACCGGCTGTGTCGAGA 1200
QY 541 GGAATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCCGGAAG 600
Db 1201 GGAATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCCGGAAG 1260
QY 601 TAAAGACGAAAGCCTTTCCTGAGCGTGGGAGGCAAGCTCTTCTCATGAGCGGAA 660
Db 1261 TAAAGACGAAAGCCTTTCCTGAGCGTGGGAGGCAAGCTCTTCTCATGAGCGGAA 1320
QY 661 ATGGAACCTTAATTTCCCGTTCCTCCCAACAGCCCGCGAGAGTGACTCTCAAG 720
Db 1321 ATGGAACCTTAATTTCCCGTTCCTCCCAACAGCCCGCGAGAGTGACTCTCAAG 1380
QY 721 ACCCGGAGAGTCAAGTTGGCCAAATCCGTGCGGCGCGCTCTCTTTAAAGCCGA 780
Db 1381 ACCCGGAGAGTCAAGTTGGCCAAATCCGTGCGGCGCGCTCTCTTTAAAGCCGA 1440
QY 781 CTCGCCGCGAGCGCAACGGGTTGCGAGGGGTGGGCTGGAGGGGTGGCCATTTT 840
Db 1441 CTCGCCGCGAGCGCAACGGGTTGCGAGGGGTGGGCTGGAGGGGTGGCCATTTT 1500
QY 841 TGTCTAACCTTAACCTGAAGAGGCGCTA 867
Db 1501 TGTCTAACCTTAACCTGAAGAGGCGCTA 1527

RESULT 3
US-08-482-115B-3
; Sequence 3, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: VILLEPOTTEAU, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000803US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-482-115B-3
Query Match 97.9%; Score 848.6; DB 1; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.6e-274;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 AGCTACTCGAGAGGCTGAGACACAGAAATCGCTTGAACCCGGGAGGCAAGGTGGAGT 60
Db 662 AGCTACTCGAGAGGCTGAGACACAGAAATCGCTTGAACCCGGGAGGCAAGGTGGAGT 720
QY 61 AGCCGAGATCAGCCCACTAGATCCATCCAGGCTGGGCGAAGAGCAAGTCCGCTCA 120
Db 721 AGCCGAGATCAGCCCACTAGATCCATCCAGGCTGGGCGAAGAGCAAGTCCGCTCA 780
QY 121 AAAAAAAAAATGTTACAAATTTATGATGATTTACTCCCTCTTTTAACTCAACAGACA 180
Db 781 AAAAAAAAAATGTTACAAATTTATGATGATTTACTCCCTCTTTTAACTCAACAGACA 840
QY 181 CAGCACTACTTTAAAGCAAAAGTCAATGATGAAAGCGCTTCTTCTTAATTAAGGAG 240
Db 841 CAGCACTACTTTAAAGCAAAAGTCAATGATGAAAGCGCTTCTTCTTAATTAAGGAG 900
QY 241 ATTCACTCTTAAGATTAATTAATGATGATTAAGTCACTGATTAAGGCAATCCCTGCTCA 300
Db 901 ATTCACTCTTAAGATTAATTAATGATGATTAAGTCACTGATTAAGGCAATCCCTGCTCA 960
QY 301 AGGAGAGCTGAGAGAGGCAATCTAAGAAAAAGGGGAGGAGGTTGAACTCGAGCGCATC 360
Db 961 AGGAGAGCTGAGAGAGGCAATCTAAGAAAAAGGGGAGGAGGTTGAACTCGAGCGCATC 1020
QY 361 CCACTAGAGCCGAGACAAGTTTGTCTGATGATGATGATGATGATGATGATGATGATGAT 420
Db 1021 CCACTAGAGCCGAGACAAGTTTGTCTGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 421 AGTTCTCCAAAAAATGATGATGATCAAACTAGAAATTAATGATGATGATGATGATGATGAT 480
Db 1081 AGTTCTCCAAAAAATGATGATGATCAAACTAGAAATTAATGATGATGATGATGATGATGAT 1140
QY 481 AATCTTCCTGTAATTCATTTTAAAGTAGTCAGATGAAACCGGCTGTGTCGAGA 540
Db 1141 AATCTTCCTGTAATTCATTTTAAAGTAGTCAGATGAAACCGGCTGTGTCGAGA 1200
QY 541 GGAATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCCGGAAG 600
Db 1201 GGAATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCCGGAAG 1260
QY 601 TAAAGACGAAAGCCTTTCCTGAGCGTGGGAGGCAAGCTCTTCTCATGAGCGGAA 660
Db 1261 TAAAGACGAAAGCCTTTCCTGAGCGTGGGAGGCAAGCTCTTCTCATGAGCGGAA 1320
QY 661 ATGGAACCTTAATTTCCCGTTCCTCCCAACAGCCCGCGAGAGTGACTCTCAAG 720
Db 1321 ATGGAACCTTAATTTCCCGTTCCTCCCAACAGCCCGCGAGAGTGACTCTCAAG 1380
QY 721 ACCCGGAGAGTCAAGTTGGCCAAATCCGTGCGGCGCGCTCTCTTTAAAGCCGA 780
Db 1381 ACCCGGAGAGTCAAGTTGGCCAAATCCGTGCGGCGCGCTCTCTTTAAAGCCGA 1440
QY 781 CTCGCCGCGAGCGCAACGGGTTGCGAGGGGTGGGCTGGAGGGGTGGCCATTTT 840
Db 1441 CTCGCCGCGAGCGCAACGGGTTGCGAGGGGTGGGCTGGAGGGGTGGCCATTTT 1500
QY 841 TGTCTAACCTTAACCTGAAGAGGCGCTA 867
Db 1501 TGTCTAACCTTAACCTGAAGAGGCGCTA 1527

RESULT 4
US-08-660-678A-3
; Sequence 3, Application US/08660678A
; Patent No. 5837857

GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-660-678A-3

Query Match 97.9%; Score 848.6; DB 2; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.6e-274;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

1 ACCTACTCAGAGGCTGAGACAGAGATCGCTTGAAACCGGAGGAGGAGGTGCAAGT 60
662 AGCTACTCAGAGGCTGAGACAGAGATCGCTTGAAACCGGAGGAGGTGCAAGT 720
61 AGCCGAGATCAGCCAGCTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
721 AGCCGAGATCAGCCAGCTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780
121 AAAAAAAAAAGTAACTAATTAATGATGATGATTAACCTCTTTTAACTCAAGACA 180
781 AAAAAAAAAAGTAACTAATTAATGATGATGATTAACCTCTTTTAACTCAAGACA 840
181 CAGCACTACTTAAAGCAAGTCAATGATTGAAAGCGCTTTCTTCTTAATAAAGGAG 240
841 CAGCACTACTTAAAGCAAGTCAATGATTGAAAGCGCTTTCTTCTTAATAAAGGAG 900
241 ATTGAGTCTTAAGATTAATTAATGATGATGATTAACCTGATTAAAGCACTCTGCTCA 300
901 ATTGAGTCTTAAGATTAATTAATGATGATGATTAACCTGATTAAAGCACTCTGCTCA 960
301 AGGAGAGGCTGAGAGGAGTCTTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
961 AGGAGAGGCTGAGAGGAGTCTTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020

361 CCACAGAGCCGAGACAGAGATTTGCTGTAGTCAAGTCTGCTGGAGATCTATTTTACAA 420
1021 CCACAGAGCCGAGACAGAGATTTGCTGTAGTCAAGTCTGCTGGAGATCTATTTTACAA 1080
421 AGTCTCCAAAAAAGTGTATGATCAAACTGGAATTAATGATGATGATGATGATGATGAT 480
1081 AGTCTCCAAAAAAGTGTATGATCAAACTGGAATTAATGATGATGATGATGATGATGAT 1140
481 AATCTCTCTGTAATTCATTTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 540
1141 AATCTCTCTGTAATTCATTTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 1200
541 GGATGAAAAAAGGCTCTGATTAACCTGATGATGATGATGATGATGATGATGATGATGAT 600
1201 GGATGAAAAAAGGCTCTGATTAACCTGATGATGATGATGATGATGATGATGATGATGAT 1260
601 TAAAGACCAAAAGCTTTCCGAGAGTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
1261 TAAAGACCAAAAGCTTTCCGAGAGTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
661 ATGAACTTTAATTTCCCGTTCCCGCCCAACCAAGCCCGCGAGAGAGTACTCTCAGAG 720
1321 ATGAACTTTAATTTCCCGTTCCCGCCCAACCAAGCCCGCGAGAGAGTACTCTCAGAG 1380
721 AGCCGAGAGTCAAGCTTGCCCAATCCGTGGGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
1381 AGCCGAGAGTCAAGCTTGCCCAATCCGTGGGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
781 CTCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
1441 CTCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
841 TGTCTAACCTTAAGTGAAGAGGCGTA 867
1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527

RESULT 5
US-08-472-802C-4
Sequence 4, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820


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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-802C-4

Query Match
Best Local Similarity 97.9%; Score 848.6; DB 2; Length 2426;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTGAGAGGCTGAGACAGAGATCGCTTGAACCCGGAGGAGAGGTTGAGTG 60
DB 662 AGCTACTGAGAGGCTGAGACAGAGATCGCTTGAACCCGGAGGAGAGGTTGAGTG 720
QY 61 AGCCGAGATCAGCCCTAGACTCCATCCAGCCTGGGCGAAGAGCAAGTCCGTCTCA 120
DB 721 AGCCGAGATCAGCCCTAGACTCCATCCAGCCTGGGCGAAGAGCAAGTCCGTCTCA 780
QY 121 AAAAAAAAAATGTTCAATTTATGTTGATTAATCTCCCTCTTTTACCTCATCAGACA 180
DB 781 AAAAAAAAAATGTTCAATTTATGTTGATTAATCTCCCTCTTTTACCTCATCAGACA 840
QY 181 CAGCACTACTTTAAAGCAAGTCATGATTGAACCGCTTTCTTCTAATAAAGGAG 240
DB 841 CAGCACTACTTTAAAGCAAGTCATGATTGAACCGCTTTCTTCTAATAAAGGAG 900
QY 241 ATTGCTCTTAAAGATTATATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 901 ATTGCTCTTAAAGATTATATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 301 AGGAGAGCTGGAGAGGATCTTAGSAAAAAGGGGCGAGGTTGAACTCGGAGCGATC 360
DB 961 AGGAGAGCTGGAGAGGATCTTAGSAAAAAGGGGCGAGGTTGAACTCGGAGCGATC 1020
QY 361 CCACTGAGCGGAGACAGATTCCTGATGATGATGATGATGATGATGATGATGATG 420
DB 1021 CCACTGAGCGGAGACAGATTCCTGATGATGATGATGATGATGATGATGATGATG 1080
QY 421 AGTTCTCCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 1081 AGTTCTCCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 481 AATCTCTCTGATGATTCATTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 540
DB 1141 AATCTCTCTGATGATTCATTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1200
QY 541 GGATGAAAAAAGGCGCTCTGATGATGATGATGATGATGATGATGATGATGATG 600
DB 1201 GGATGAAAAAAGGCGCTCTGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 601 TAAAGACGCAAGCTTTCCCGGAGCTGGGAGAGGCAAGTCTTCTCATAGCCGGA 660
DB 1261 TAAAGACGCAAGCTTTCCCGGAGCTGGGAGAGGCAAGTCTTCTCATAGCCGGA 1320
QY 661 ATGGAACCTTAATTTCCCGTCCCGCAACGCGCGCGCGAGAGTCACTCAAGAG 720
DB 1321 ATGGAACCTTAATTTCCCGTCCCGCAACGCGCGCGCGAGAGTCACTCAAGAG 1380
QY 721 AGCCGAGAGTCAAGCTTGGCCCAATCGTGGCGGTGGCGCGCTCTTTAATAGCGA 780
DB 1381 AGCCGAGAGTCAAGCTTGGCCCAATCGTGGCGGTGGCGCGCTCTTTAATAGCGA 1440
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DB 1441 CTCGCCCGGAGCGCACCGGGTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
QY 841 TGTCTTAACCTTAATGAGAAAGGCGGTA 867
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DB 1501 TGTCTTAACCTTAATGAGAAAGGCGGTA 1527

RESULT 6
US-08-714-482-1
Sequence 1, Application US/08714482
Patent No. 5972605
GENERAL INFORMATION:
APPLICANT: Valleponteau, Bryant
APPLICANT: Harley, Calvin
TITLE OF INVENTION: Assays for Regulators of Mammalian
TITLE OF INVENTION: Telomerase Expression
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,482
CLASSIFICATION: 435
FILING DATE: 16-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/521,634
FILING DATE: 31-AUG-1995
APPLICATION NUMBER: US 08/482,115
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00860US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..2426
OTHER INFORMATION: /note="SauIII-HindIII fragment
OTHER INFORMATION: containing htr sequences as well as
OTHER INFORMATION: transcription regulatory sequences"
US-08-714-482-1

Query Match
Best Local Similarity 97.9%; Score 848.6; DB 2; Length 2426;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTGAGAGGCTGAGACAGAGATCGCTTGAACCCGGAGGAGAGGTTGAGTG 60
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QY 481 AAATCTCTGTGAATTCATTTTAAAGTAGTGAACGCGCTGTGTGCGAGA 540
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DB 1141 AAATCTCTGTGAATTCATTTTAAAGTAGTGAACGCGCTGTGTGCGAGA 1200
| | | | |
QY 541 GGAATGAAAAAGGCGCTGTGAATCCTCAAGTTAGTTCACTTTAAAGAGTCCGAG 600
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DB 1201 GGAATGAAAAAGGCGCTGTGAATCCTCAAGTTAGTTCACTTTAAAGAGTCCGAG 1260
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QY 601 TAAAGACGCAAAACCTTTCCCGGACGTCGGAAGGCGCAAGTCTTCTCATAGCCGGA 660
| | | | |
DB 1261 TAAAGACGCAAAACCTTTCCCGGACGTCGGAAGGCGCAAGTCTTCTCATAGCCGGA 1320
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QY 661 ATGAACTTTAATTTCCCGTCCCGCCCAACGAGCCCGCGAGAGTGACTCTCAAGAG 720
| | | | |
DB 1321 ATGAACTTTAATTTCCCGTCCCGCCCAACGAGCCCGCGAGAGTGACTCTCAAGAG 1380
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QY 721 AGCCGAGAGTCAAGTGTGCGCAATCCGTGCGGCGCGCTCCCTTTAATAGCGGA 780
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DB 1381 AGCCGAGAGTCAAGTGTGCGCAATCCGTGCGGCGCGCTCCCTTTAATAGCGGA 1440
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QY 781 CTGCCCCGAGCGCACCGGCTTGCAGAGGCTGGGCTTGGAAGGCTGCGCATTTT 840
| | | | |
DB 1441 CTGCCCCGAGCGCACCGGCTTGCAGAGGCTGGGCTTGGAAGGCTGCGCATTTT 1500
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QY 841 TGTCTAACCTTAAGTGAAGAGGCGTA 867
| | | | |
DB 1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527
| | | | |

RESULT 8
US-09-060-523-3
Sequence 3, Application US/09060523
GENERAL INFORMATION:
APPLICANT: Villedieu, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-Apr-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storer, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:

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SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-060-523-3

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Query Match 97.9%; Score 848.6; DB 3; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.6e-274;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 1 AGCTACTGAGAGGCTGAGACAGAGATCGCTGAACCGGAGGCAAGTGTGAGTG 60
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DB 662 AGCTACTGAGAGGCTGAGACAGAGATCGCTGAACCGGAGGCAAGTGTGAGTG 720
| | | | |
QY 61 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAGAGCAAGTCCGTCTCA 120
| | | | |
DB 721 AGCCGAGATCAGGCCACTAGACTCCATCCAGCCTGGGCGAAGAGCAAGTCCGTCTCA 780
| | | | |
QY 121 AAAAAAAAAATGTTAATTTATGTTGATTAATCTCCCTCTTTTAACTCATAGACA 180
| | | | |
DB 781 AAAAAAAAAATGTTAATTTATGTTGATTAATCTCCCTCTTTTAACTCATAGACA 840
| | | | |
QY 181 CAGCACTACTTTAAAGCAAGTCAATGATGTAAGAGCGCTTCTTCTAATAAAGGAG 240
| | | | |
DB 841 CAGCACTACTTTAAAGCAAGTCAATGATGTAAGAGCGCTTCTTCTAATAAAGGAG 900
| | | | |
QY 241 ATTCACTCTTAAGATTAATTAATGATGTTACACTTGAATTAAGCAATCTCTGCTCA 300
| | | | |
DB 901 ATTCACTCTTAAGATTAATTAATGATGTTACACTTGAATTAAGCAATCTCTGCTCA 960
| | | | |
QY 301 AGGAGAGCTGAGAGAGCAATTTCTAAGAGAAAAAGGCGAGGTTGGAATCTCGAGCATC 360
| | | | |
DB 961 AGGAGAGCTGAGAGAGCAATTTCTAAGAGAAAAAGGCGAGGTTGGAATCTCGAGCATC 1020
| | | | |
QY 361 CCACTGAGCGGAGACAAAGATTCGCTGTAGTCAAGTCTGCGGAATCTAATTTACAA 420
| | | | |
DB 1021 CCACTGAGCGGAGACAAAGATTCGCTGTAGTCAAGTCTGCGGAATCTAATTTACAA 1080
| | | | |
QY 421 AGTTCTCAAAAAATGTGATGATCAAACTAGGAATTAATGTTCTGTTAGGCCCTA 480
| | | | |
DB 1081 AGTTCTCAAAAAATGTGATGATCAAACTAGGAATTAATGTTCTGTTAGGCCCTA 1140
| | | | |
QY 481 AAATCTCTGTGAATTCATTTTAAAGTAGTGAACGCGCTGTGTGCGAGA 540
| | | | |
DB 1141 AAATCTCTGTGAATTCATTTTAAAGTAGTGAACGCGCTGTGTGCGAGA 1200
| | | | |
QY 541 GGAATGAAAAAGGCGCTGTGAATCCTCAAGTTAGTTCACTTTAAAGAGTCCGAG 600
| | | | |
DB 1201 GGAATGAAAAAGGCGCTGTGAATCCTCAAGTTAGTTCACTTTAAAGAGTCCGAG 1260
| | | | |
QY 601 TAAAGACGCAAAACCTTTCCCGGACGTCGGAAGGCGCAAGTCTTCTCATAGCCGGA 660
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DB 1261 TAAAGACGCAAAACCTTTCCCGGACGTCGGAAGGCGCAAGTCTTCTCATAGCCGGA 1320
| | | | |
QY 661 ATGAACTTTAATTTCCCGTCCCGCCCAACGAGCCCGCGAGAGTGACTCTCAAGAG 720
| | | | |
DB 1321 ATGAACTTTAATTTCCCGTCCCGCCCAACGAGCCCGCGAGAGTGACTCTCAAGAG 1380
| | | | |
QY 721 AGCCGAGAGTCAAGTGTGCGCAATCCGTGCGGCGCGCTCCCTTTAATAGCGGA 780
| | | | |
DB 1381 AGCCGAGAGTCAAGTGTGCGCAATCCGTGCGGCGCGCTCCCTTTAATAGCGGA 1440
| | | | |
QY 781 CTGCCCCGAGCGCACCGGCTTGCAGAGGCTGGGCTTGGAAGGCTGCGCATTTT 840
| | | | |
DB 1441 CTGCCCCGAGCGCACCGGCTTGCAGAGGCTGGGCTTGGAAGGCTGCGCATTTT 1500
| | | | |
QY 841 TGTCTAACCTTAAGTGAAGAGGCGTA 867
| | | | |
DB 1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527
| | | | |

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RESULT 9
US-09-057-351-3
; Sequence 3, Application US/09057351
; Patent No. 6548298
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-057-351-3

Query Match      97.9%; Score 848.6; DB 4; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.6e-274;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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; Sequence 1, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhunda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-485-778-1

Query Match      96.3%; Score 834.6; DB 2; Length 2425;
Best Local Similarity 99.0%; Pred. No. 8.5e-270;
Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

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DB AGCCGAGATCAGCCCACTAGACTCAATCCAGCCTGGGCGAAGAGAGAGCTCCGTCTCA 780
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DB AAAAAAAAAATCTTCAATTATGTTGATTAATCTCCCTCTTTTAACTCATGAAGACA 900
QY 181 CAGCACTACTTTAAAGCAAGTGAATGTAAGAGCGCTTCTTCTATATAAAGGAG 240
DB CAGCACTACTTTAAAGCAAGTGAATGTAAGAGCGCTTCTTCTATATAAAGGAG 900
QY 241 ATTCACTCTTAAGATTAAATGATGATGATTAATCACTTGAATTAAGCACTCTCTCA 300
DB ATTCACTCTTAAGATTAAATGATGATGATTAATCACTTGAATTAAGCACTCTCTCA 960
QY 301 AGGAGAGCTGAGAGAGGATTTAAAGAAAAAGGGGAGGGTTGAACTCGAGCGCATC 360
DB AGGAGAGCTGAGAGAGGATTTAAAGAAAAAGGGGAGGGTTGAACTCGAGCGCATC 1020
QY 961 AGGAGAGCTGAGAGAGGATTTAAAGAAAAAGGGGAGGGTTGAACTCGAGCGCATC 1020
DB AGGAGAGCTGAGAGAGGATTTAAAGAAAAAGGGGAGGGTTGAACTCGAGCGCATC 420
QY 361 CCACTGAGCGGAGAGCAAGATTCGTGCTGATGCTGCTGCGGAGATCATTTTCAAA 420
DB CCACTGAGCGGAGAGCAAGATTCGTGCTGATGCTGCTGCGGAGATCATTTTCAAA 1080
QY 1021 CCACTGAGCGGAGAGCAAGATTCGTGCTGATGCTGCTGCGGAGATCATTTTCAAA 1080
DB CCACTGAGCGGAGAGCAAGATTCGTGCTGATGCTGCTGCGGAGATCATTTTCAAA 1140
QY 421 AGTTCTCAAAAAAATGATGATCAAAACTAGAGATTAAGTGTCTGTCTTAAAGCCCTTA 480
DB AGTTCTCAAAAAAATGATGATCAAAACTAGAGATTAAGTGTCTGTCTTAAAGCCCTTA 1140
QY 481 AATCTCTCTGATGATTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB AATCTCTCTGATGATTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1141 AATCTCTCTGATGATTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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QY 541 GGATGAGAAAAAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB GGATGAGAAAAAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
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DB GGATGAGAAAAAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 601 TAAAGAGCAAGAGCTTTCCCGGAGCTGGGAGAGGCAAGTCTCTCTCATAGCCGGA 660
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QY 781 CTCGCCCGCAGAGCAACCGGTTGC---GAGAGGTGGGCTTGGAGAGGGGTGGCCAT 836
DB CTCGCCCGCAGAGCAACCGGTTGC---GAGAGGTGGGCTTGGAGAGGGGTGGCCAT 1500
QY 837 TTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCT 867
DB TTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCT 1531

RESULT 11
US-08-520-550A-1
Sequence 1, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Valleponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-550A-1
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[illegible]

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1  TITLE OF INVENTION:  Telomerase Expression
2  NUMBER OF SEQUENCES:  2
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Townsend and Townsend and Crew LLP
5  STREET:  Two Embarcadero Center, Eighth Floor
6  CITY:  San Francisco
7  STATE:  California
8  COUNTRY:  USA
9  ZIP:  94111-3834
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Floppy disk
12 COMPUTER:  IBM PC compatible
13 OPERATING SYSTEM:  PC-DOS/MS-DOS
14 SOFTWARE:  PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER:  US/08/714,482
17 FILING DATE:  16-SEP-1996
18 CLASSIFICATION:  435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:  US 08/521,634
21 FILING DATE:  31-AUG-1995
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER:  US 08/482,115
24 FILING DATE:  07-JUN-1995
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:  US 08/472,802
27 FILING DATE:  07-JUN-1995
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:  US 08/330,123
30 FILING DATE:  27-OCT-1994
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER:  US 08/272,102
33 FILING DATE:  07-JUL-1994
34 ATTORNEY/AGENT INFORMATION:
35 NAME:  Storella, John R.
36 REGISTRATION NUMBER:  32,944
37 REFERENCE/DOCKET NUMBER:  015389-00860US
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE:  (415) 576-0200
40 TELEFAX:  (415) 576-0300
41 INFORMATION FOR SEQ ID NO:  2:
42 SEQUENCE CHARACTERISTICS:
43     LENGTH:  981 base pairs
44     TYPE:  nucleic acid
45     STRANDEDNESS:  single
46     TOPOLOGY:  linear
47 MOLECULE TYPE:  DNA (genomic)
48 FEATURE:
49     NAME/KEY:  -
50     LOCATION:  1..981
51     OTHER INFORMATION:  /note="PsiI fragment containing hTR
52     OTHER INFORMATION:  sequence"
53 US-08-714-482-2
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55 Query Match          38.5%; Score 334; DB 2; Length 981;
56 Best local Similarity 100.0%; Pred. No. 1.3e-101;
57 Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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63 Db 61 TGGGAAGTAAAGCCCAAGCCTTTCCCGACGTGCGGAAGGGCAACGTCCTTCTCATG 120
64
65 QY 654 GCCGGAATGGAACCTTTATTTCCGTTCCCGCCCAACACAGCCGCGCGAGAGATGATC 713
66 Db 121 GCCGGAATGGAACCTTTATTTCCGTTCCCGCCCAACACAGCCGCGCGAGAGATGATC 180
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68 QY 714 TACAGAGACCGCGAGAGTCAAGTTCGACCAATCCGTGCGTGGCGCGCGCTCCCTTAT 773
69 Db 181 TACAGAGACCGCGAGAGTCAAGTTCGACCAATCCGTGCGTGGCGCGCGCTCCCTTAT 240

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QY 774 AGCCGACTCGCCGCGAGCGACCGGGTTGCGAGGGGTGGCCCTGGGAGGGGTGGTGC 833
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Db 241 AGCCGACTCGCCGCGAGCGACCGGGTTGCGAGGGGTGGCCCTGGGAGGGGTGGTGC 300
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QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGCTA 867
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Db 301 CATTTTGTCTAACCTTAAGTGAAGGCGCTA 334
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RESULT 13
US-08-710-249-5
; Sequence 5, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 267..715
; OTHER INFORMATION: /product= "hTR"
; OTHER INFORMATION: /note= "hTR transcript serves as
; OTHER INFORMATION: template in the telomerase
; OTHER INFORMATION: ribonucleoprotein"
; US-08-710-249-5
Query Match 38.4%; Score 333; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.8e-101;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 61 TCGGAAGTAAAGCGCAAGGCTTTTCCGGAAGTGGGAAGGCAAGCTTCTTCATG 120
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QY 654 GCCGGAATGAACTTAATTTCCGTTCCCGCCCAACGAGCCCGCGAGAGTGAATC 713
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Db 241 AGCCGACTCGCCGCGAGCGACCGGGTTGCGAGGGGTGGCCCTGGGAGGGGTGGTGC 300
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QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGCTA 867
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Db 301 CATTTTGTCTAACCTTAAGTGAAGGCGCTA 334
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RESULT 14
US-09-220-157A-5
; Sequence 5, Application US/09220157A
; Patent No. 6300110
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,157A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

FEATURE:
 NAME/KEY: misc_RNA
 LOCATION: 267-715
 OTHER INFORMATION: /product= "hTR"
 OTHER INFORMATION: /note= "hTR transcript serves as
 OTHER INFORMATION: template in the telomerase
 OTHER INFORMATION: ribonucleoprotein"
 US-09-220-157A-5

Query Match 38.4%; Score 333; DB 3; Length 981;
 Best Local Similarity 99.7%; Pred. No. 2.8e-101;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAAGATGATAAAAAAGCCCTGTGATACCTCAAGTAGTTTCACTTTAAAGAG 593
 DB 1 CTGCAAGATGATAAAAAAGCCCTGTGATACCTCAAGTAGTTTCACTTTAAAGAG 60
 QY 594 TCGAAGTAAAGACGCAAGCCTTTCCCGACGTGCGAAGGCAACGTCCTTCATG 653
 DB 61 TCGAAGTAAAGACGCAAGCCTTTCCCGACGTGCGAAGGCAACGTCCTTCATG 120
 QY 654 GCCGAAATGGAACCTTAATTTCCGTTCCCGCAACGACCCCGGAGAGTGAATC 713
 DB 121 GCCGAAATGGAACCTTAATTTCCGTTCCCGCAACGACCCCGGAGAGTGAATC 180
 QY 714 TCACGAGAGCCGCGAGAGTCACTTGGCCCAATCCGTGCGGTGCGGCGGCTCCCTTAT 773
 DB 181 TCACGAGAGCCGCGAGAGTCACTTGGCCCAATCCGTGCGGTGCGGCGGCTCCCTTAT 240
 QY 774 AAGCCGACTCGCCCGGACGCAACGCGGTTGCGAGGGTGGGCTTGGAGGGGTGGTGC 833
 DB 241 AAGCCGACTCGCCCGGACGCAACGCGGTTGCGAGGGTGGGCTTGGAGGGGTGGTGC 300
 QY 834 CATTITTTGTCTAACCTTAACCTGAGAGGGCGTA 867
 DB 301 CATTITTTGTCTAACCTTAACCTGAGAGGGCGTA 334

RESULT 15

US-08-770-565-1

Sequence 1, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo

APPLICANT: Mu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinlich, Scott L.

TITLE OF INVENTION: Methods for Detecting the RNA Component of

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 981 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-770-565-1

Query Match 38.3%; Score 332.4; DB 2; Length 981;
 Best Local Similarity 99.7%; Pred. No. 4.4e-101;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAAGATGATAAAAAAGCCCTGTGATACCTCAAGTAGTTTCACTTTAAAGAG 593
 DB 1 CTGCAAGATGATAAAAAAGCCCTGTGATACCTCAAGTAGTTTCACTTTAAAGAG 60
 QY 594 TCGAAGTAAAGACGCAAGCCTTTCCCGACGTGCGAAGGCAACGTCCTTCATG 653
 DB 61 TCGAAGTAAAGACGCAAGCCTTTCCCGACGTGCGAAGGCAACGTCCTTCATG 120
 QY 654 GCCGAAATGGAACCTTAATTTCCGTTCCCGCAACGACCCCGGAGAGTGAATC 713
 DB 121 GCCGAAATGGAACCTTAATTTCCGTTCCCGCAACGACCCCGGAGAGTGAATC 180
 QY 714 TCACGAGAGCCGCGAGAGTCACTTGGCCCAATCCGTGCGGTGCGGCGGCTCCCTTAT 773
 DB 181 TCACGAGAGCCGCGAGAGTCACTTGGCCCAATCCGTGCGGTGCGGCGGCTCCCTTAT 240
 QY 774 AAGCCGACTCGCCCGGACGCAACGCGGTTGCGAGGGTGGGCTTGGAGGGGTGGTGC 833
 DB 241 AAGCCGACTCGCCCGGACGCAACGCGGTTGCGAGGGTGGGCTTGGAGGGGTGGTGC 300
 QY 834 CATTITTTGTCTAACCTTAACCTGAGAGGGCGTA 867
 DB 301 CATTITTTGTCTAACCTTAACCTGAGAGGGCGTA 334

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 Job time: 192.318 secs